



SEQUENCE LISTING

<110> Sleeman, Matthew
Murison, Greg

<120> Fibroblast Growth Factor Receptors and Methods for Their Use

<130> 11000.1037c5

<150> U.S. 09/823,038

<151> 2001-03-28

<150> U.S. 09/383,586

<151> 1999-08-26

<150> U.S. 09/276,268

<151> 1999-03-25

<150> PCT/NZ00/00015

<151> 2000-02-18

<150> U.S. 60/221,216

<151> 2000-07-25

<150> U.S. 10/157,444

<151> 2000-05-28

<150> PCT/NZ03/00105

<151> 2003-05-27

<160> 145

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 384

<212> DNA

<213> Mouse

<220>

<221> misc_feature

<222> (1)...(384)

<223> n = A,T,C or G

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tgtgggtggc	cagaagtttg	tgggtgttgc	cacgggtgat	gtgtgggtcac	ggcctgatgg	180
ctcctacctc	aacaagctgc	tcctctctcg	ggcccggccag	gatgatgctg	gcatgtacat	240
ctgcctaggt	gcaaatacca	tgggctacag	tttccgtagc	gccttcctca	ctgtattacc	300
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<210> 2

<211> 1967

<212> DNA

<213> Mouse

<400> 2

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gcctggggccg	cactgtgcgg	ctacagtgcc	cagtggaggg	ggaccaccca	ccgttgacca	360
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cacatgttta	aacgtgtaaa	cgtgtgcaca	actgcacaca	caacctgaga	aaccttcagg	1920
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ggtagcgccg	ccccgcccag	gccggggccc	ggggcgcggg	gggcgggatg	cggcgcccgg	180
ggcagcgatg	accgcgtcgc	gctgctcagg	ggcccggctc	tgaccccggt	gcctgctgcg	240
cgcccccgcg	ctgatccctg	tcgagcgtct	acgcgcctcg	cttcctttgc	ctggagctcg	300
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cctgagtggc	gtccagtcca	gctcccagtg	accgcgcccc	tgcttcagggt	ccgaccggcg	420
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cggcgcgaga	tgatattagt	ccagggaagg	agagccctgg	gccagggtgg	tcttcggggg	540
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cagcatgtcc	actatcagtg	ctaaatacag	cgaatctcca	agcactgtgt	cctgaggtag	1680
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agatggcgga	caaggtggtc	ccacggcagg	tggccggctg	ggccgcactg	tgcggtgca	180
gtgccagtgg	agggggaccc	gccgccgctg	accatgtgga	ccaaggatgg	ccgcaccatc	240
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aagtgcgtgg	ccagcgggca	ccctcggccc	gacatcacgt	ggatgaagga	cgaccaggcc	600
ttgacgcgcc	cagaggccgc	tgagcccagg	aagaagaagt	ggacactgag	cctgaagaac	660
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cgccacaact	ccaccatcga	tgtggggcgg	cagaagtctg	tggtgctgcc	cacgggtgac	960
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<220>
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Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile
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Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu
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Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser
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<210> 6

<211> 529

<212> PRT

<213> Mouse

<400> 6

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Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
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Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50					55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
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Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
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Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
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Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
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Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
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Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
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			340					345					350			
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<210> 7
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<400> 7																
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Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Pro	Gly	Pro	Pro	Met	
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Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	
305					310					315					320	
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	
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Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	
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<400> 8																
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Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	
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Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly	Pro	Asp
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Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg
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Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro
			180					185					190		
Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn
		195					200					205			
Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Arg
		210				215						220			
Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr
225					230					235					240
Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val
				245					250					255	
Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val
			260					265					270		
Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly
		275					280					285			
Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu
		290				295						300			
Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys
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Pro	Leu														

<210> 9
 <211> 1423
 <212> DNA
 <213> Mouse

<400> 9	
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agcttgaaga acctgaagcc tgaagacagt ggcaagtaca cgtgccgtgt atctaacaag	180
gccggtgcca tcaacgccac ctacaaagtg gatgtaatcc gtgagtgggt ggtctgtggt	240
aggacagggg cccgtgggtgc ctaaaactgt gctgacatgt ttgtttttcc ttggcttaga	300
gcggactcgt tccaagcctg tgctcacagg gacacaccct gtgaacacaa cggtggactt	360
cgggtgggaca acgtccttcc agtgcaaggt gcgcagtgc gtgaagcctg tgatccagt	420
gctgaagcgg gtggagtacg gctccgaggg acgccacaac tccaccattg atgtgggtgg	480
ccagaagtgt gtggtgttgc ccacgggtga tgtgtggtca cggcctgatg gctcctacct	540
caacaagctg ctcatctctc gggcccgcga ggatgatgct ggcattgtaca tctgcctagg	600
tgcaaatacc atgggctaca gtttccgtag cgccttctc actgtattac cagggtgtgtg	660
tgtgggctgc ccaccccatg tttactctca gtctctacca ttgggtctggg ctgtcctggg	720
gttccccaat gtccacttag caagtggggc ctccctatcc ttttccctc gttgtgggtt	780
atccttgcct catagggagt tcaggggtgc tgcccatata gttcacattt gggctggttg	840
ccccattaat atagggacat tctgtcccct actcttctc ttaatctctc ttgcagaccc	900
caaacctcca gggcctccta tggcttcttc atcgatcatc acaagcctgc catggcctgt	960
ggtgatcggc atcccagctg gtgctgtctt catcctaggc actgtgctgc tctggctttg	1020
ccagaccaag aagaagccat gtgccccagc atctacactt cctgtgcctg ggcacgtcc	1080
cccagggaca tcccagagaac gcagtgggtga caaggacctg cctcatttg ctgtgggcat	1140
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tggccccaag ctgtacccca agctatacac agatgtgcac acacacacac atacacacac	1260
ctgcactcac acgtctcat gtggagggca aggttcatca acaccagcat gtccactatc	1320
agtgcataat acagcgaatc tccaagcact gtgtcctgag gtaggcataat gggggccaag	1380

gcaacagggtt gggagaattg agaacaatgg aggaagagta tct 1423

<210> 10
<211> 35
<212> DNA
<213> Mouse

<400> 10
cgggatccag gccatggcag gcttgtggat gacga 35

<210> 11
<211> 37
<212> DNA
<213> Mouse

<400> 11
ccgctcgagt agatactctt cctccattgt tctcatt 37

<210> 12
<211> 18
<212> DNA
<213> Mouse

<400> 12
ctgtgcggct caagtgtg 18

<210> 13
<211> 373
<212> PRT
<213> Mouse

<400> 13
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Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
20 25 30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
35 40 45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
50 55 60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65 70 75 80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
85 90 95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
100 105 110
Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
115 120 125
Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg
130 135 140
Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val
145 150 155 160
Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro
165 170 175
Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu Thr His Leu Glu Ala
180 185 190
Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys

1	5	10	15
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg			
	20	25	30
Pro Asp Gly Ser Tyr			
35			

<210> 16
 <211> 1515
 <212> DNA
 <213> Human

<400> 16

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtg	agggggaccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
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gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccagggg	aggagagcct	ggggcccagc	agctcctctg	gggtcaaga	ggaccccgcc	420
agccagcagt	gggcacgacc	gcgcttcaca	cagccctcca	agatgaggcg	ccgggtgatc	480
gcacggcccc	tgggtagctc	cgtgcggctc	aagtgcgtgg	ccagcgggca	ccctcggccc	540
gacatcacgt	ggatgaagga	cgaccaggcc	ttgacgcgcc	cagaggccgc	tgagcccagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcggcccg	aggacagcgg	caaatacacc	660
tgccgcgtgt	cgaaccgcgc	gggcgccatc	aacgccacct	acaagggtga	tgtgatccag	720
cggacccggt	ccaagcccgt	gctcacaggc	acgcaccccg	tgaacacgac	ggtggacttc	780
ggggggacca	cgtccttcca	gtgcaagggt	cgcagcgacg	tgaagccggt	gatccagtgg	840
ctgaagcgcg	tggagtacgg	cgccgagggc	cgccacaact	ccaccatcga	tgtgggcggc	900
cagaagtttg	tgggtgctgc	cacgggtgac	gtgtgggtcg	ggcccagcgg	ctcctacctc	960
aataagctgc	tcataccccg	tgcccgccag	gacgatgcgg	gcatgtacat	ctgccttggc	1020
gccaacacca	tgggctacag	cttcgcgacg	gccttcctca	ccgtgctgcc	agacccaaaa	1080
ccgcaagggc	cacctgtggc	ctcctcgtcc	tcggccacta	gcctgccgtg	gcccgtggtc	1140
atcggcatcc	cagccggcgc	tgtcttcac	ctgggcaccc	tgctcctgtg	gctttgccag	1200
gcccagaaga	agccgtgcac	ccccgcgcct	gcccctcccc	tgctggggca	ccgcccgcgc	1260
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cacacacaca	cacactctca	cacacactca	cacgtggagg	gcaagggtcca	ccagcacatc	1500
cactatcagt	gctag					1515

<210> 17
 <211> 504
 <212> PRT
 <213> Human

<400> 17

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	20
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg	
	35
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr	
	50
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu	
65	70
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val	
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	90
	95

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<210> 18
<211> 1161
<212> DNA
<213> Human
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<400> 18
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gcccggctgg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgctg    180
accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg    240
ccgcagggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag    300
gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggatgacatt    360
agcccaggga aggagagcct ggggcccagc agctcctctg ggggtcaaga ggaccccgcc    420
agccagcagt gggcacgacc gcgcttcaca cagccctcca agatgaggcg ccgggtgatc    480
gcacggccccg tgggtagctc cgtgcggctc aagtgcgtgg ccagcgggca ccctcggccc    540
gacatcacgt ggatgaagga cgaccaggcc ttgacgcgcc cagaggccgc tgagcccagg    600
aagaagaagt ggacactgag cctgaagaac ctgcggcccg aggacagcgg caaatacacc    660
tgccgcgtgt cgaaccgcgc gggcgccatc aacgccacct acaaggtgga tgtgatccac    720
ccaaaaccgc aagggccacc tgtggcctcc tcgtcctcgg ccactagcct gccgtggccc    780
gtgggtcatcg gcatcccagc cggcgtgtc ttcatacctg gcaccctgct cctgtggctt    840
tgccaggccc agaagaagcc gtgcaccccc gcgcctgccc ctccccctgcc tgggcaccgc    900
ccgccggggga cggcccgcga ccgcagcggg gacaaggacc ttccctcgtt ggccgcctc    960
agcgtgggcc ctggtgtggg gctgtgtgag gagcatgggt ctccggcagc ccccagcac    1020
ttactgggcc caggcccagt tgctggccct aagttgtacc ccaaactcta cacagacatc    1080
cacacacaca cacacacaca ctctcacaca cactcacacg tggagggcaa ggtccaccag    1140
cacatccact atcagtgcta g                                     1161

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<210> 19
<211> 386
<212> PRT
<213> Human

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<400> 19
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
          20          25          30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
          35          40          45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
          50          55          60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
65          70          75          80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
          85          90          95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
          100          105          110
Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
          115          120          125
Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
          130          135          140
Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile

          145          150          155          160
Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly
          165          170          175
His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr

          180          185          190
Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu

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<213> Human

<400> 21

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	
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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala	
			20					25					30			
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	
		35				40						45				
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	
	50					55					60					
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	
65					70					75					80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val	
				85					90					95		
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	
			100					105					110			
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly	
		115					120					125				
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	
	130					135					140					
Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	
145					150					155					160	
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	
				165					170					175		
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	
			180					185					190			
Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	
		195					200					205				
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	
	210					215					220					
Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	
225					230					235					240	
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	
			245						250					255		
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	
			260					265						270		
Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	
		275					280					285				
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	
	290					295					300					
Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	
305					310					315					320	
Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	
				325					330					335		
Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	
			340					345					350			
Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	
		355					360					365				
Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	
	370					375					380					
Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	
385					390					395					400	
Val	His	Gln	His	Ile	His	Tyr	Gln	Cys								
				405												

<210> 22

<211> 1434
 <212> DNA
 <213> Human

<400> 22
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 gcccggtctg gccgcactgt gcggctgcag tgcccagtgagg aggggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcaggggc tgaagggtgaa gcagggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggcacgaccg 360
 cgcttcacac agccctccaa gatgaggcgc cgggtgatcg cacggcccgt gggtagctcc 420
 gtgcggctca agtgcggtggc cagcggggcac cctcggcccg acatcacgtg gatgaaggac 480
 gaccaggcct tgacgcgccc agaggccgct gagcccagga agaagaagtg gacactgagc 540
 ctgaagaacc tgcggccgga ggacagcggc aaatacacct gccgcgtgtc gaaccgcgcg 600
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 ctcacaggca cgcaccccgt gaacacgacg gtggacttcg gggggaccac gtccttccag 720
 tgcaagggtg gcagcgacgt gaagccgggt atccagtggc tgaagcgcgt ggagtacggc 780
 gccgagggcc gccacaactc caccatcgat gtggggcggcc agaagtttgt ggtgctgccc 840
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 gcccgccagg acgatgcggg catgtacatc tgccttgggc ccaacaccat gggctacagc 960
 ttccgcagcg ccttcctcac cgtgctgcca gacccaaaac cgcaagggcc acctgtggcc 1020
 tcctcgtcct cggccactag cctgccgtgg cccgtgggtca tcggcatccc agccggcgct 1080
 gtcttcatcc tgggcaccct gctcctgtgg ctttgccagg ccagaagaa gccgtgcacc 1140
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 ggagacaagg accttccctc gttggccgcc ctcagcgtg gccctgggtg ggggctgtgt 1260
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 cctaagttgt accccaaact ctacacagac atccacacac acacacacac acactctcac 1380
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<210> 23
 <211> 477
 <212> PRT
 <213> Human

<400> 23
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 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
 115 120 125
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
 130 135 140
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
 145 150 155 160
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys

				165					170					175			
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr		
			180						185				190				
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys		
		195					200					205					
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr		
	210					215					220						
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln		
225				230					235						240		
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg		
			245					250				255					
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly		
			260				265					270					
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro		
	275					280					285						
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp		
	290				295						300						
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser		
305				310				315							320		
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly		
			325					330						335			
Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val		
		340					345					350					
Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu		
	355					360					365						
Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala		
	370			375							380						
Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser		
385				390					395						400		
Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly		
			405					410					415				
Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu		
		420					425					430					
Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr		
	435					440					445						
Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His		
	450				455						460						
Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His	Tyr	Gln	Cys					
465				470						475							

<210> 24
 <211> 1242
 <212> DNA
 <213> Human

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tcctctgggg gtcaagagga ccccgccagc cagcagtggg cacgaccgcg cttcacacag	180
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caccccgtga acacgacggt ggacttcggg gggaccacgt ccttccagtg caaggtgcgc	540
agcgacgtga agccggtgat ccagtggctg aagcgcgtgg agtacggcgc cgagggccgc	600
cacaactcca ccatcgatgt gggcggccag aagtttgtgg tgctgcccac gggtgacgtg	660

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gatgcgggca	tgtacatctg	ccttggcgcc	aacaccatgg	gctacagctt	ccgcagcgcc	780
ttcctcaccg	tgctgccaga	cccaaaaccg	caagggccac	ctgtggcctc	ctcgtcctcg	840
gccactagcc	tgccgtggcc	cgtgggtcatc	ggcatcccag	ccggcgctgt	cttcatacctg	900
ggcaccctgc	tcttgtggct	ttgccaggcc	cagaagaagc	cgtgcacccc	cgcgcctgcc	960
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tctccggcag	ccccccagca	cttactgggc	ccaggcccag	ttgctggccc	taagttgtac	1140
cccaaactct	acacagacat	ccacacacac	acacacacac	actctcacac	acactcacac	1200
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<210> 25

<211> 413

<212> PRT

<213> Human

<400> 25

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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	
			20					25					30			
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	
		35					40					45				
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	
	50					55					60					
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	
65					70				75						80	
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	
				85					90					95		
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	
			100					105					110			
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	
		115					120					125				
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	
	130					135					140					
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	
145					150					155					160	
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	
			165						170					175		
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	
		180						185					190			
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	
	195						200					205				
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	
	210					215					220					
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	
225					230					235					240	
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	
			245						250					255		
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln	Gly	
		260						265					270			
Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	
	275						280					285				
Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	
	290					295					300					
Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	
305				310					315						320	

Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser
				325					330					335	
Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly
			340					345					350		
Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu
		355					360					365			
Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr
	370					375					380				
Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His
385					390					395					400
Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His	Tyr	Gln	Cys			
				405					410						

<210> 26
 <211> 876
 <212> DNA
 <213> Human

<400> 26

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accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcggtga	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
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ctgcctgggc	accgcccgcc	ggggacggcc	cgcgaccgca	gcggagacaa	ggaccttccc	660
tcgttggccg	ccctcagcgc	tggccctggt	gtggggctgt	gtgaggagca	tgggtctccg	720
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<210> 27
 <211> 291
 <212> PRT
 <213> Human

<400> 27

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35				40						45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75						80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
			85					90					95		
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
			115				120					125			

Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
130						135					140				
Asp	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr
145					150					155					160
Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe
				165					170					175	
Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro
			180					185					190		
Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly
		195					200					205			
Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala
	210					215					220				
Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro
225					230					235					240
Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys
			245						250					255	
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His
			260					265					270		
Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His
		275					280					285			
Tyr	Gln	Cys													
	290														

<210> 28
 <211> 1080
 <212> DNA
 <213> Human

<400> 28

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ccgcaggggg	tgaagggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggcacgaccg	360
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gaccaggcct	tgacgcgccc	agaggccgct	gagcccagga	agaagaagtg	gacactgagc	540
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ggcgccatca	acgccaccta	caagggtggat	gtgatccacc	caaaaccgca	agggccacct	660
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ctgtgtgagg	agcatgggtc	tccggcagcc	ccccagcact	tactgggccc	aggcccagtt	960
gctggcccta	agttgtaccc	caaactctac	acagacatcc	acacacacac	acacacacac	1020
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<210> 29
 <211> 359
 <212> PRT
 <213> Human

<400> 29

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala

		20						25					30				
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg		
		35					40					45					
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr		
	50					55					60						
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu		
65					70					75					80		
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val		
			85						90				95				
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr		
			100					105					110				
Thr	Leu	Val	Val	Leu	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met		
		115					120					125					
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys		
	130					135					140						
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp		
145					150					155					160		
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys		
			165					170					175				
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr		
		180					185						190				
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys		
	195					200					205						
Val	Asp	Val	Ile	His	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser		
	210					215					220						
Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala		
225					230					235					240		
Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala		
			245					250						255			
Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His		
			260					265					270				
Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro		
	275						280					285					
Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu		
	290					295					300						
His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val		
305					310					315					320		
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His		
			325					330					335				
Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	His		
		340						345					350				
Gln	His	Ile	His	Tyr	Gln	Cys											
		355															

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 <211> 1149
 <212> DNA
 <213> Human

<400> 30	
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gcccggctgg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgctg	180
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gccaccaacg gcttcggcag ccttagcgct aactacacc tcgtcgtgct ggagcggacc	360
cgttccaagc ccgtgctcac aggcacgcac cccgtgaaca cgacggtgga cttcgggggg	420

accacgtcct	tccagtgcaa	ggtgcgcgagc	gacgtgaagc	cggatgatcca	gtggctgaag	480
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tttgtggtgc	tgcccacggg	tgacgtgtgg	tcgcggcccg	acggctccta	cctcaataag	600
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<210> 31
 <211> 382
 <212> PRT
 <213> Human

<400> 31

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			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35					40					45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75					80	
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85					90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105						110	
Thr	Leu	Val	Val	Leu	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly
		115					120						125		
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe
	130						135					140			
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys
145					150					155				160	
Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val
				165				170						175	
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg
			180					185					190		
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
		195					200					205			
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr
210						215					220				
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Gln
225					230					235				240	
Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro
				245					250					255	
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu
			260					265					270		
Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro
		275					280					285			

Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
130						135					140				
Val	Asp	Val	Ile	His	Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser
145					150					155					160
Ser	Ser	Ala	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala
				165					170					175	
Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala
			180					185					190		
Gln	Lys	Lys	Pro	Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His
	195						200					205			
Arg	Pro	Pro	Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro
210						215					220				
Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu
225				230						235				240	
His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val
				245					250					255	
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His
			260					265					270		
Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	Val	His
	275						280					285			
Gln	His	Ile	His	Tyr	Gln	Cys									
290						295									

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 <211> 957
 <212> DNA
 <213> Human

<400> 34	
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agcttccgca gcgccttcct caccgtgctg ccagacccaa aaccgcaagg gccacctgtg	540
gcctcctcgt cctcggccac tagcctgccg tggcccgtgg tcatcggcac ccagccggc	600
gctgtcttca tcctgggcac cctgctcctg tggctttgcc agggccagaa gaagccgtgc	660
acccccgcgc ctgcccctcc cctgcctggg caccgcccgc cggggacggc ccgcgaccgc	720
agcggagaca aggaccttcc ctcgttggcc gccctcagcg ctggccctgg tgtggggctg	780
tgtgaggagc atgggtctcc ggcagccccc cagcacttac tgggcccagg ccagttgct	840
ggcctaagt tgtaccccaa actctacaca gacatccaca cacacacaca cacacactct	900
cacacacact cacacgtgga gggcaaggct caccagcaca tccactatca gtgctag	957

<210> 35
 <211> 318
 <212> PRT
 <213> Human

<400> 35	
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu	
1 5 10 15	
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly	
20 25 30	
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro	

ccgccgggga	cggccccgca	ccgcagcgga	gacaaggacc	ttccctcggt	ggccgccctc	960
agcgctggcc	ctggtgtggg	gctgtgtgag	gagcatgggt	ctccggcagc	ccccagcac	1020
ttactgggcc	caggcccagt	tgctggccct	aagttgtacc	ccaaactcta	cacagacatc	1080
cacacacaca	cacacacaca	ctctcacaca	cactcacacg	tggagggcaa	ggtccaccag	1140
cacatccact	atcagtgcta	g				1161

<210> 37
 <211> 386
 <212> PRT
 <213> Human

<400> 37

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr
			20					25					30		
Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser
		35					40					45			
Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile
	50					55					60				
Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu
65				70						75					80
Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu
			85					90					95		
Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile
			100					105					110		
Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro
		115					120					125			
Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly
	130					135					140				
Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile
145				150						155					160
Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser
			165					170						175	
Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp
			180					185					190		
Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr
	195					200						205			
Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn
	210					215					220				
Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp
225				230						235					240
Pro	Lys	Pro	Gln	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser
			245					250					255		
Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile
			260					265					270		
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	Cys
	275						280					285			
Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr
	290					295					300				
Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu
305					310					315					320
Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala
			325					330					335		
Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu
		340						345					350		
Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser

Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu
195 200 205
Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro
210 215 220
Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
225 230 235 240
His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val
245 250 255
His Gln His Ile His Tyr Gln Cys
260

<210> 40
<211> 603
<212> DNA
<213> Human

<400> 40
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tcctctgggg gtcaagagga ccccgccagc cagcagtggg acccaaaacc gcaagggcca 180
cctgtggcct cctcgtcctc ggccactagc ctgccgtggc ccgtgggtcat cggcatccca 240
gccggcgctg tcttcatcct gggcaccctg ctctgtggc tttgccaggc ccagaagaag 300
ccgtgcaccc ccgcgcctgc ccctcccctg cctggggcacc gcccgccggg gacggcccgc 360
gaccgcagcg gagacaagga ccttccctcg ttggccgccc tcagcgctgg ccctggtgtg 420
gggctgtgtg aggagcatgg gtctccggca gccccccagc acttactggg cccaggccca 480
gttgctggcc ctaagttgta ccccaaactc tacacagaca tccacacaca cacacacaca 540
cactctcaca cacactcaca cgtggagggc aaggtccacc agcacatcca ctatcagtgc 600
tag 603

<210> 41
<211> 200
<212> PRT
<213> Human

<400> 41
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
20 25 30
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
35 40 45
Ala Ser Gln Gln Trp Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser
50 55 60
Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro
65 70 75 80
Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln
85 90 95
Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly
100 105 110
His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu
115 120 125
Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu
130 135 140
Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro
145 150 155 160
Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr
165 170 175

His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys Val
180 185 190
His Gln His Ile His Tyr Gln Cys
195 200

<210> 42
<211> 807
<212> DNA
<213> Human

<400> 42
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ccggccgccg ccgcccgcgc acgaccgcgc ttcacacagc cctccaagat gaggcgccgg 120
gtgatcgcac ggcccgtggg tagctccgtg cggctcaagt gcgtggccag cgggcaccct 180
cggcccgcaca tcacgtggat gaaggacgac caggccttga cgcgcccgaga ggccgctgag 240
cccaggaaga agaagtggac actgagcctg aagaacctgc ggccggagga cagcggcaaa 300
tacacctgcc gcgtgtcgaa ccgcgcgggc gccatcaacg ccacctacaa ggtggatgtg 360
atccacccaa aaccgcaagg gccacctgtg gcctcctcgt cctcggccac tagcctgccg 420
tggcccgtgg tcatcggcat ccagcccggc gctgtcttca tcctggggcac cctgctcctg 480
tggctttgcc aggccagaa gaagccgtgc accccgcgc ctgcccctcc cctgcctggg 540
caccgcccgc cggggacggc ccgcgaccgc agcggagaca aggaccttcc ctcgttggcc 600
gccctcagcg ctggccctgg tgtggggctg tgtgaggagc atgggtctcc ggcagcccc 660
cagcacttac tgggcccagg ccagttgct ggccctaagt tgtaccccaa actctacaca 720
gacatccaca cacacacaca cacacactct cacacacact cacacgtgga gggcaaggtc 780
caccagcaca tccactatca gtgctag 807

<210> 43
<211> 268
<212> PRT
<213> Human

<400> 43
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
20 25 30
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
35 40 45
Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
50 55 60
Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
65 70 75 80
Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
85 90 95
Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
100 105 110
Asn Ala Thr Tyr Lys Val Asp Val Ile His Pro Lys Pro Gln Gly Pro
115 120 125
Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val
130 135 140
Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu
145 150 155 160
Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro
165 170 175
Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly
180 185 190

Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val
	195						200					205			
Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu
	210					215					220				
Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr
225					230					235					240
Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val
			245						250					255	
Glu	Gly	Lys	Val	His	Gln	His	Ile	His	Tyr	Gln	Cys				
			260						265						

<210> 44
 <211> 876
 <212> DNA
 <213> Human

<400> 44

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gtgaacacga	cggtggactt	cggggggacc	acgtccttcc	agtgcagggt	gcgcagcgac	180
gtgaagccgg	tgatccagtg	gctgaagcgc	gtggagtacg	gcgccgaggg	ccgccacaac	240
tccaccatcg	atgtgggagg	ccagaagttt	gtggtgctgc	ccacgggtga	cgtgtggtcg	300
cggcccgcag	gctcctacct	caataagctg	ctcatcaccc	gtgcccgcga	ggacgatgcg	360
ggcatgtaca	tctgccttgg	cgccaacacc	atgggctaca	gcttccgcag	cgccttcctc	420
accgtgctgc	cagacccaaa	accgcaaggg	ccacctgtgg	cctcctcgtc	ctcggccact	480
agcctgccgt	ggcccgtggt	catcggcctc	ccagccggcg	ctgtcttcat	cctgggcacc	540
ctgctcctgt	ggctttgcca	ggcccagaag	aagccgtgca	cccccgcgcc	tgcccctccc	600
ctgcctgggc	accgcccgcg	ggggacggcc	cgcgaccgca	gcggagacaa	ggaccttccc	660
tcgttggccg	ccctcagcgc	tggccctggt	gtggggctgt	gtgaggagca	tgggtctccg	720
gcagcccccc	agcacttact	gggcccaggc	ccagttgctg	gccctaagtt	gtaccccaaa	780
ctctacacag	acatccacac	acacacacac	acacactctc	acacacactc	acacgtggag	840
ggcaagggtcc	accagcacat	ccactatcag	tgctag			876

<210> 45
 <211> 291
 <212> PRT

<213> Human

<400> 45

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Glu	Arg	Thr	Arg	Ser	Lys
			20					25					30		
Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly
		35					40					45			
Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val
		50				55					60				
Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn
65					70					75					80
Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly
			85						90					95	
Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile
			100					105					110		
Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala
		115					120					125			
Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro

130	135	140
Asp Pro Lys Pro Gln Gly Pro Pro Val Ala Ser Ser Ser Ser Ala Thr		
145	150	155
Ser Leu Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe		
	165	170
Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro		
	180	185
Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly		
	195	200
Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala		
	210	215
Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro		
225	230	235
Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys		
	245	250
Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr His Thr His Thr His		
	260	265
Ser His Thr His Ser His Val Glu Gly Lys Val His Gln His Ile His		
	275	280
Tyr Gln Cys		285
290		

<210> 46
 <211> 522
 <212> DNA
 <213> Human

<400> 46	
atgacgccga gccccctgtt gctgctcctg ctgccgccgc tgctgctggg ggccttccca	60
ccggccgccg ccgcccagaga cccaaaaccg caagggccac ctgtggcctc ctcgtcctcg	120
gccactagcc tgccgtggcc cgtgggtcatc ggcattcccag ccggcgctgt cttcatcctg	180
ggcaccctgc tcctgtggct ttgccaggcc cagaagaagc cgtgcacccc cgcgcctgcc	240
cctcccctgc ctgggcaccg cccgccgggg acggcccgcg accgcagcgg agacaaggac	300
cttccctcgt tggccgccct cagcgctggc cctgggtgtgg ggctgtgtga ggagcatggg	360
tctccggcag cccccagca cttactgggc ccaggcccag ttgctggccc taagttgtac	420
cccaaactct acacagacat ccacacacac acacacacac actctcacac acactcacac	480
gtggagggca aggtccacca gcacatccac tatcagtgtc ag	522

<210> 47
 <211> 173
 <212> PRT
 <213> Human

<400> 47
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Pro Lys Pro Gln Gly
20 25 30
Pro Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val
35 40 45
Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu
50 55 60
Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala
65 70 75 80
Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser
85 90 95
Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly

			100					105					110				
Val	Gly	Leu	Cys	Glu	Glu	His	Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu		
		115					120					125					
Leu	Gly	Pro	Gly	Pro	Val	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr		
	130					135					140						
Thr	Asp	Ile	His	Thr	His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His		
145					150					155					160		
Val	Glu	Gly	Lys	Val	His	Gln	His	Ile	His	Tyr	Gln	Cys					
			165					170									

<210> 48
 <211> 1072
 <212> DNA
 <213> Human

<400> 48

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtgg	agggggaccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggc	tgaaggatga	gcaggtggag	cgaggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccagggg	aggagagcct	ggggccccgac	agctcctctg	gggtcaaga	ggaccccgcc	420
agccagcagt	gggcacgacc	gcgcttcaca	cagccctcca	agatgaggcg	ccgggtgatc	480
gcacggcccc	tgggtagctc	cgtgcggctc	aagtgcgtgg	ccagcgggca	ccctcggccc	540
gacatcacgt	ggatgaagga	cgaccaggcc	ttgacgcgcc	cagaggccgc	tgagcccagg	600
aagaagaagt	ggacactgag	cctgaagaac	ctgcggccgg	aggacagcgg	caaatacacc	660
tgccgcgtgt	cgaaccgcgc	gggcgccatc	aacgccacct	acaaggatga	tgtgatccag	720
cggacccggt	ccaagcccgt	gctcacaggc	acgcaccccg	tgaacacgac	ggtggacttc	780
ggggggacca	cgtccttcca	gtgcaagggtg	cgcagcgacg	tgaagccggt	gatccagtgg	840
ctgaagcgcg	tggagtacgg	cgccgagggc	cgccacaact	ccaccatcga	tgtgggcggc	900
cagaagtttg	tgggtgctgcc	cacgggtgac	gtgtggtcgc	ggcccagcgg	ctcctacctc	960
aataagctgc	tcatcacccg	tgcccgccag	gacgatgcgg	gcatgtacat	ctgccttggc	1020
gccaacacca	tgggctacag	cttccgcagc	gccttcctca	ccgtgctgcc	ag	1072

<210> 49
 <211> 357
 <212> PRT
 <213> Human

<400> 49

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5				10					15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20					25					30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35				40						45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75						80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
			85						90					95	
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100					105					110		
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
			115				120					125			

Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
130						135					140				
Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile
145					150					155					160
Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly
				165					170					175	
His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu	Thr
			180					185					190		
Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu
		195					200					205			
Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser
	210					215					220				
Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln
225					230					235					240
Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr
			245						250					255	
Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser
		260						265						270	
Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala
	275						280					285			
Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val
	290					295					300				
Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu
305					310					315					320
Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr
			325						330					335	
Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe
		340						345					350		
Leu	Thr	Val	Leu	Pro											
		355													

<210> 50
 <211> 718
 <212> DNA
 <213> Human

<400> 50	
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gcccggctgg gccgcactgt gcggctgcag tgcccagtg agggggaccc gccgccgctg	180
accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg	240
ccgcagggggc tgaagggtgaa gcagggtggag cgggaggatg ccggcgtgta cgtgtgcaag	300
gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggatgacatt	360
agcccaggga aggagagcct ggggcccagc agctcctctg ggggtcaaga ggaccccgcc	420
agccagcagt gggcacgacc gcgcttcaca cagccctcca agatgaggcg ccgggtgatc	480
gcacggccccg tgggtagctc cgtgcggctc aagtgcgtgg ccagcgggca ccctcggccc	540
gacatcacgt ggatgaagga cgaccaggcc ttgacgcgcc cagaggccgc tgagcccagg	600
aagaagaagt ggacactgag cctgaagaac ctgcggccgg aggacagcgg caaatacacc	660
tgccgcgtgt cgaaccgcgc gggcgccatc aacgccacct acaagggtgga tgtgatcc	718

<210> 51
 <211> 239
 <212> PRT
 <213> Human

<400> 51
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu

1	5	10	15
Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys Met Ala			
20	25	30	
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg			
35	40	45	
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr			
50	55	60	
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu			
65	70	75	80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val			
85	90	95	
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr			
100	105	110	
Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly			
115	120	125	
Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp			
130	135	140	
Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val Ile			
145	150	155	160
Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly			
165	170	175	
His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr			
180	185	190	
Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu			
195	200	205	
Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser			
210	215	220	
Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile			
225	230	235	

<210> 52
 <211> 787
 <212> DNA
 <213> Human

<400> 52

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gcccggctgg	gccgcactgt	gcggctgcag	tgcccagtg	agggggaccc	gccgccgctg	180
accatgtgga	ccaaggatgg	ccgcaccatc	cacagcggct	ggagccgctt	ccgcgtgctg	240
ccgcaggggg	tgaaggtgaa	gcaggtggag	cgggaggatg	ccggcgtgta	cgtgtgcaag	300
gccaccaacg	gcttcggcag	ccttagcgtc	aactacaccc	tcgtcgtgct	ggatgacatt	360
agcccagggg	aggagagcct	ggggccccgac	agctcctctg	ggggtcaaga	ggaccccgcc	420
agccagcagt	gggagcggac	ccgttccaag	cccgtgctca	caggcacgca	ccccgtgaac	480
acgacggtgg	acttcggggg	gaccacgtcc	ttccagtgca	aggtgcgcag	cgacgtgaag	540
ccggtgatcc	agtggctgaa	gcgcgtggag	tacggcgccg	agggccgcca	caactccacc	600
atcgatgtgg	gcggccagaa	gtttgtggtg	ctgcccacgg	gtgacgtgtg	gtcgcggccc	660
gacggctcct	acctcaataa	gctgctcatc	acccgtgccc	gccaggacga	tgcgggcatg	720
tacatctgcc	ttggcgccaa	caccatgggc	tacagcttcc	gcagcgcctt	cctcaccgtg	780
ctgccag						787

<210> 53
 <211> 262
 <212> PRT
 <213> Human

<400> 53

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5				10					15		
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Gly	Pro	Pro	Lys	Met	Ala
			20				25						30		
Asp	Lys	Val	Val	Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg
		35				40						45			
Leu	Gln	Cys	Pro	Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr
	50					55					60				
Lys	Asp	Gly	Arg	Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu
65					70				75						80
Pro	Gln	Gly	Leu	Lys	Val	Lys	Gln	Val	Glu	Arg	Glu	Asp	Ala	Gly	Val
				85				90					95		
Tyr	Val	Cys	Lys	Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr
			100				105						110		
Thr	Leu	Val	Val	Leu	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Leu	Gly
		115				120						125			
Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp
	130					135					140				
Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
145					150					155					160
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
			165						170					175	
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
			180				185						190		
Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
		195					200					205			
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
	210					215					220				
Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
225					230					235					240
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
			245						250					255	
Phe	Leu	Thr	Val	Leu	Pro										
			260												

<210> 54
 <211> 991
 <212> DNA
 <213> Human

<400> 54	
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gcccggtggg gccgcactgt gcggctgcag tgcccagtgagg ggggggaccc gccgccgctg	180
accatgtgga ccaaggatgg ccgcaccatc cacagcggtt ggagccgctt ccgcgtgctg	240
ccgcaggggc tgaaggatga gcaggtggag cgggaggatg ccggcggtga cgtgtgcaag	300
gccaccaacg gcttcggcag ccttagcgct aactacacc tcgtcggtgct ggcacgaccg	360
cgcttcacac agccctccaa gatgaggcgc cgggtgatcg cacggcccgt gggtagctcc	420
gtgcggctca agtgcggtggc cagcgggcac cctcggcccc acatcacgtg gatgaaggac	480
gaccaggcct tgacgcgccc agaggccgct gagcccagga agaagaagtg gacactgagc	540
ctgaagaacc tgcggccgga ggacagcggc aaatacacct gccgcgtgtc gaaccgcgcg	600
ggcgccatca acgccaccta caaggtggat gtgatccagc ggaccggttc caagcccgtg	660
ctcacaggca cgcaccccgt gaacacgacg gtggacttcg gggggaccac gtccttccag	720
tgcaaggtgc gcagcgacgt gaagccggtg atccagtggc tgaagcgcgt ggagtacggc	780
gccgagggcc gccacaactc caccatcgat gtgggcggcc agaagtgtgt ggtgctgccc	840
acgggtgacg tgtggtcgcg gcccgacggc tcctacctca ataagctgct catcaccgct	900
gcccgccagg acgatgcggg catgtacatc tgccttggcg ccaacaccat gggctacagc	960

ttccgcagcg ccttcctcac cgtgctgccca g

991

<210> 55
<211> 330
<212> PRT
<213> Human

<400> 55
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
20 25 30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
35 40 45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
50 55 60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
65 70 75 80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
85 90 95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
100 105 110
Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
115 120 125
Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
130 135 140
Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
145 150 155 160
Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys
165 170 175
Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
180 185 190
Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
195 200 205
Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr
210 215 220
His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln
225 230 235 240
Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg
245 250 255
Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly
260 265 270
Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro
275 280 285
Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp
290 295 300
Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser
305 310 315 320
Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
325 330

<210> 56
<211> 799
<212> DNA
<213> Human

<400> 56

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tcctctgggg	gtcaagagga	ccccgccagc	cagcagtggg	cacgaccgcg	cttcacacag	180
ccctccaaga	tgaggcgccg	ggtgatcgca	cggcccgtgg	gtagctccgt	gcggctcaag	240
tgcgtaggcca	gcgggcaccc	tcggcccgc	atcacgtgga	tgaaggacga	ccaggccttg	300
acgcgcccag	aggccgctga	gcccaggaag	aagaagtgga	cactgagcct	gaagaacctg	360
cggccggagg	acagcggcaa	atacacctgc	cgcgtgtcga	accgcgcggg	cgccatcaac	420
gccacctaca	aggtggatgt	gatccagcgg	acccgtttcca	agcccgtgct	cacaggcacg	480
caccccgtga	acacgacggg	ggacttcggg	gggaccacgt	ccttccagt	caaggtgcgc	540
agcgacgtga	agccggtgat	ccagtggctg	aagcgcgtgg	agtacggcgc	cgagggccgc	600
cacaactcca	ccatcgatgt	gggcggccag	aagtttgtgg	tgctgcccac	gggtgacgtg	660
tggtcgcggc	ccgacggctc	ctacctcaat	aagctgctca	tcacccgtgc	ccgccaggac	720
gatgcgggca	tgtacatctg	ccttggcgcc	aacaccatgg	gctacagctt	ccgcagcgcc	780
ttcctcaccg	tgctgccag					799

<210> 57

<211> 266

<212> PRT

<213> Human

<400> 57

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu	
1				5					10				15			
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	
			20					25					30			
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	
		35					40					45				
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	
	50					55					60					
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	
65					70				75						80	
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	
				85					90					95		
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	
			100					105					110			
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	
	115						120					125				
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	
	130					135					140					
Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	
145					150					155					160	
His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	
			165						170					175		
Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	
		180						185					190			
Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	
	195						200					205				
Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	
	210					215					220					
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	Asp	
225					230					235					240	
Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	
			245					250						255		
Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro							
			260					265								

<210> 58

<211> 433
 <212> DNA
 <213> Human

<400> 58
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 gcccggtctg gccgcactgt gcggctgcag tgcccagtgg aggggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcaggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggatgacatt 360
 agcccaggga aggagagcct ggggcccgcac agctcctctg ggggtcaaga ggaccccgcc 420
 agccagcagt ggg 433

<210> 59
 <211> 144
 <212> PRT
 <213> Human

<400> 59
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Asp Asp Ile Ser Pro Gly Lys Glu Ser Leu Gly
 115 120 125
 Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140

<210> 60
 <211> 637
 <212> DNA
 <213> Human

<400> 60
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 gcccggtctg gccgcactgt gcggctgcag tgcccagtgg aggggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcaggggc tgaaggtgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggcacgaccg 360
 cgcttcacac agccctccaa gatgaggcgc cgggtgatcg cacggcccgt gggtagctcc 420
 gtgcggctca agtgcggtggc cagcggggcac cctcggcccg acatcacgtg gatgaaggac 480
 gaccaggcct tgacgcgccc agaggccgct gagcccagga agaagaagtg gacactgagc 540
 ctgaagaacc tgcggccgga ggacagcggc aaatacacct gccgcgtgtc gaaccgcgcg 600
 ggcgccatca acgccaccta caaggtggat gtgatcc 637

<210> 61
 <211> 212
 <212> PRT
 <213> Human

<400> 61
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met
 115 120 125
 Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys
 130 135 140
 Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr Trp Met Lys Asp
 145 150 155 160
 Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro Arg Lys Lys Lys
 165 170 175
 Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp Ser Gly Lys Tyr
 180 185 190
 Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys
 195 200 205
 Val Asp Val Ile
 210

<210> 62
 <211> 706
 <212> DNA
 <213> Human

<400> 62
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 gcccggtggt gccgcactgt gcggctgcag tgcccagtggt aggggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcgggt ggagccgctt ccgcgtgctg 240
 ccgcagggggc tgaagggtgaa gcagggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct ggagcggacc 360
 cgttccaagc ccgtgctcac aggcacgcac cccgtgaaca cgacgggtgga cttcggggggg 420
 accacgtcct tccagtgcaa ggtgcgcagc gacgtgaagc cggatgatcca gtggctgaag 480
 cgcgtggagt acggcgccga gggccgccac aactccacca tcgatgtggg cggccagaag 540
 tttgtggtgc tgcccacggg tgacgtgtgg tcgcggcccg acggctccta cctcaataag 600
 ctgctcatca cccgtgcccg ccaggacgat gcgggcatgt acatctgcct tggcgccaac 660
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<210> 63
 <211> 235
 <212> PRT

<213> Human

<400> 63

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
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Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
          20          25          30
Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
          35          40          45
Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
          50          55          60
Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
65          70          75          80
Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
          85          90          95
Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
          100          105          110
Thr Leu Val Val Leu Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly
          115          120          125
Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe
          130          135          140
Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys
145          150          155          160
Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val
          165          170          175
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg
          180          185          190
Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln
          195          200          205
Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr
210          215          220
Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
225          230          235
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<210> 64

<211> 445

<212> DNA

<213> Human

<400> 64

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ccggccgccg ccgcccgaga tgacattagc ccaggggaagg agagcctggg gcccgacagc      120
tcctctgggg gtcaagagga ccccgccagc cagcagtggg caccgaccgc cttcacacag      180
ccctccaaga tgaggcgccg ggtgatcgca cggcccgtgg gtagctccgt gcggctcaag      240
tgcgtagcca gcgggcaccc tcggcccgcac atcacgtgga tgaaggacga ccaggccttg      300
acgcgcccag aggccgctga gccaggaag aagaagtgga cactgagcct gaagaacctg      360
cggccggagg acagcggcaa atacacctgc cgcgtgtcga accgcgcggg cgccatcaac      420
gccacctaca aggtggatgt gatcc                                     445
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<210> 65

<211> 148

<212> PRT

<213> Human

<400> 65

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Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1          5          10          15
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Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly
			20					25					30		
Lys	Glu	Ser	Leu	Gly	Pro	Asp	Ser	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro
		35					40					45			
Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met
	50					55					60				
Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys
65					70					75					80
Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp
				85					90					95	
Asp	Gln	Ala	Leu	Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys
			100					105					110		
Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr
		115					120					125			
Thr	Cys	Arg	Val	Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys
	130					135					140				
Val	Asp	Val	Ile												
145															

<210> 66
 <211> 514
 <212> DNA
 <213> Human

<400> 66	
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ccggccgccg ccgcccgcga tgacattagc ccaggggaagg agagcctggg gcccgcacagc	120
tcctctgggg gtcaagagga ccccgccagc cagcagtggg agcggacccg ttccaagccc	180
gtgctcacag gcacgcaccc cgtgaacacg acggtggact tcggggggac cacgtccttc	240
cagtgcgaagg tgcgcagcga cgtgaagccg gtgatccagt ggctgaagcg cgtggagtac	300
ggcgccgagg gccgccacaa ctccaccatc gatgtgggcg gccagaagtt tgtggtgctg	360
cccacgggtg acgtgtggtc gcggcccgac ggctcctacc tcaataagct gctcatcacc	420
cgtgcccgcc aggacgatgc gggcatgtac atctgccttg gcgccaacac catgggctac	480
agcttccgca gcgccttctt caccgtgctg ccag	514

<210> 67
 <211> 171
 <212> PRT
 <213> Human

<400> 67	
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu	
1 5 10 15	
Gly Ala Phe Pro Pro Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly	
20 25 30	
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro	
35 40 45	
Ala Ser Gln Gln Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly	
50 55 60	
Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe	
65 70 75 80	
Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys	
85 90 95	
Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val	
100 105 110	
Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg	
115 120 125	

Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln
130 135 140
Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr
145 150 155 160
Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
165 170

<210> 68
<211> 718
<212> DNA
<213> Human

<400> 68
atgacgccga gccccctggt gctgctcctg ctgccgccgc tgctgctggg ggccttccca 60
ccggccgccg ccgcccgcgc acgaccgcgc ttcacacagc cctccaagat gaggcgccgg 120
gtgatcgcac ggcccgctggg tagctccgtg cggctcaagt gcgtggccag cgggcaccct 180
cggcccgcaca tcacgtggat gaaggacgac caggccttga cgcgccaga ggccgctgag 240
cccaggaaga agaagtggac actgagcctg aagaacctgc ggccggagga cagcggcaaa 300
tacacctgcc gcgtgtcgaa ccgcgcgggc gccatcaacg ccacctacaa ggtggatgtg 360
atccagcggg cccgttccaa gcccgctgctc acaggcacgc accccgtgaa cacgacgggtg 420
gacttcgggg ggaccacgtc cttccagtgc aaggtgcgca gcgacgtgaa gccggtgatc 480
cagtggctga agcgcgtgga gtacggcgcc gagggccgcc acaactccac catcgatgtg 540
ggcggccaga agtttgtggg gctgcccacg ggtgacgtgt ggtcgcggcc cgacggctcc 600
tacctcaata agctgctcat caccctgcc cgccaggacg atgcgggcat gtacatctgc 660
cttggcgcca acaccatggg ctacagcttc cgcagcgcct tcctcaccgt gctgccag 718

<210> 69
<211> 239
<212> PRT
<213> Human

<400> 69
Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
20 25 30
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
35 40 45
Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
50 55 60
Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
65 70 75 80
Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
85 90 95
Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
100 105 110
Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro
115 120 125
Val Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly
130 135 140
Thr Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile
145 150 155 160
Gln Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser
165 170 175
Thr Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp
180 185 190
Val Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr

	195		200		205
Arg	Ala Arg Gln Asp Asp	Ala Gly Met Tyr Ile	Cys Leu Gly Ala Asn		
210		215	220		
Thr Met Gly Tyr Ser Phe	Arg Ser Ala Phe Leu	Thr Val Leu Pro			
225	230	235			

<210> 70
 <211> 352
 <212> DNA
 <213> Human

<400> 70
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 gcccggtctg gccgcactgt gcggctgcag tgcccagtgg agggggaccc gccgccgctg 180
 accatgtgga ccaaggatgg ccgcaccatc cacagcggct ggagccgctt ccgcgtgctg 240
 ccgcagggggc tgaaggatgaa gcaggtggag cgggaggatg ccggcgtgta cgtgtgcaag 300
 gccaccaacg gcttcggcag ccttagcgtc aactacaccc tcgtcgtgct gg 352

<210> 71
 <211> 117
 <212> PRT
 <213> Human

<400> 71
 Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
 1 5 10 15
 Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Gly Pro Pro Lys Met Ala
 20 25 30
 Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg
 35 40 45
 Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr
 50 55 60
 Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu
 65 70 75 80
 Pro Gln Gly Leu Lys Val Lys Gln Val Glu Arg Glu Asp Ala Gly Val
 85 90 95
 Tyr Val Cys Lys Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr
 100 105 110
 Thr Leu Val Val Leu
 115

<210> 72
 <211> 160
 <212> DNA
 <213> Human

<400> 72
 atgacgccga gccccctggt gctgctcctg ctgccgccgc tgctgctggg ggccttccca 60
 ccggccgccg ccgccccgaga tgacattagc ccaggggaagg agagcctggg gcccgacagc 120
 tcctctgggg gtcaagagga ccccgccagc cagcagtggg 160

<210> 73
 <211> 53
 <212> PRT
 <213> Human

<400> 73

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Asp Asp Ile Ser Pro Gly
20 25 30
Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly Gln Glu Asp Pro
35 40 45
Ala Ser Gln Gln Trp
50

<210> 74

<211> 364

<212> DNA

<213> Human

<400> 74

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gtgatcgcac ggcccgtggg tagctccgtg cggctcaagt gcgtggccag cgggcaccct 180
cggcccgcaca tcacgtggat gaaggacgac caggccttga cgcgccaga ggcgctgag 240
cccaggaaga agaagtggac actgagcctg aagaacctgc ggccggagga cagcggcaaa 300
tacacctgcc gcgtgtcgaa ccgcgcgggc gccatcaacg ccacctacaa ggtggatgtg 360
atcc 364

<210> 75

<211> 121

<212> PRT

<213> Human

<400> 75

Met Thr Pro Ser Pro Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
1 5 10 15
Gly Ala Phe Pro Pro Ala Ala Ala Ala Arg Ala Arg Pro Arg Phe Thr
20 25 30
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser
35 40 45
Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile
50 55 60
Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu
65 70 75 80
Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu
85 90 95
Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile
100 105 110
Asn Ala Thr Tyr Lys Val Asp Val Ile
115 120

<210> 76

<211> 433

<212> DNA

<213> Human

<400> 76

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ccggccgccg ccgcccgcgc gcggaccggt tccaagcccg tgctcacagg cacgcacccc 120
gtgaacacga cgggtggactt cgggggggacc acgtccttcc agtgcaagggt gcgcagcgac 180
gtgaagccgg tgatccagtg gctgaagcgc gtggagtacg gcgccgaggg ccgccacaac 240

tccaccatcg atgtgggcgg ccagaagttt gtggtgctgc ccacgggtga cgtgtggtcg	300
cggcccgacg gctcctacct caataagctg ctcatacccc gtgcccgcga ggacgatgcg	360
ggcatgtaca tctgccttgg cgccaacacc atgggctaca gcttccgcag cgccttcctc	420
accgtgctgc cag	433

<210> 77
 <211> 144
 <212> PRT
 <213> Human

<400> 77

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg	Glu	Arg	Thr	Arg	Ser	Lys
			20					25					30		
Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly
		35					40					45			
Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val
	50					55					60				
Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn
65					70					75					80
Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly
			85						90				95		
Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile
			100					105					110		
Thr	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala
		115					120					125			
Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro
	130					135					140				

<210> 78
 <211> 79
 <212> DNA
 <213> Human

<400> 78	
atgacgccga gccccctggt gctgctcctg ctgccgccgc tgctgctggg ggccttccca	60
ccggccgccg ccgcccgcag	79

<210> 79
 <211> 26
 <212> PRT
 <213> Human

<400> 79

Met	Thr	Pro	Ser	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Leu	Leu	Leu
1				5					10					15	
Gly	Ala	Phe	Pro	Pro	Ala	Ala	Ala	Ala	Arg						
			20					25							

<210> 80
 <211> 1590
 <212> DNA
 <213> Mouse

<400> 80	
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gcgcgaggac	ccccagaat	ggcagacaaa	gtggtccac	ggcaggtggc	ccgcctgggc	120
cgactgtgc	ggctacagt	cccagtggag	ggggaccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccaggggtctg	240
aaggtgaagg	aggtggaggg	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggggaag	360
gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	accagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcattca	gaggctagt	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgccatcaa	cgccacctac	aaagtggatg	taatccagcg	gactcgttcc	720
aagcctgtgc	tcacagggac	acaccctgtg	aacacaacgg	tggacttcgg	tgggacaacg	780
tccttccagt	gcaaggtgcg	cagtgcgtg	aagcctgtga	tccagtggct	gaagcgggtg	840
gagtacggct	ccgagggacg	ccacaactcc	accattgatg	tgggtggcca	gaagtttgtg	900
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atctctcggg	cccgccagga	tgatgctggc	atgtacatct	gcctaggtgc	aaataccatg	1020
ggctacagtt	tccgtagcgc	cttctcact	gtattaccag	accccaaacc	tccagggcct	1080
cctatggctt	cttcatcgtc	atccacaagc	ctgccatggc	ctgtggtgat	cggcatccca	1140
gctggtgctg	tcttcatcct	aggcactgtg	ctgctctggc	tttgccagac	caagaagaag	1200
ccatgtgccc	cagcatctac	acttcctgtg	cctgggcatc	gtcccccagg	gacatcccga	1260
gaacgcagt	gtgacaagga	cctgccctca	ttggctgtgg	gcataatgtga	ggagcatgga	1320
tccgccatgg	ccccccagca	catectggcc	tctggctcaa	ctgctggccc	caagctgtac	1380
cccaagctat	acacagatgt	gcacacacac	acacatacac	acacctgcac	tcacacgctc	1440
tcatgtggag	ggcaagggtc	atcaacacca	gcattgtccac	tatcagtgtc	aaatacagcg	1500
aatctccaag	cactgtgtcc	tgaggtaggc	atttgggggc	caaggcaaca	ggttgggaga	1560
attgagaaca	atggaggaag	agtatcttag				1590

<210> 81

<211> 529

<212> PRT

<213> Mouse

<400> 81

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
			20					25				30		Val
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
			35				40					45		Pro
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
			50			55					60			Arg
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65					70				75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
				85				90					95	Lys
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
			100					105					110	Ile
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly
		115					120					125		Ser
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro
		130				135					140			Arg
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro
145					150					155				160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg
				165				170					175	Pro
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu
			180					185					190	Ala

Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	
		195					200					205				
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	
	210					215					220					
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	
225					230					235					240	
Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	
				245					250					255		
Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	
			260					265					270			
Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	
	275					280						285				
Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	
	290					295					300					
Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	
305					310					315					320	
Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	
				325					330					335		
Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	
			340					345					350			
Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	
	355					360						365				
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	
	370					375					380					
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	
385					390					395					400	
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	
				405					410					415		
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	
			420					425					430			
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	
	435						440					445				
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	
	450					455					460					
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	
465					470					475					480	
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	
				485					490					495		
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	
			500					505				510				
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	
	515						520					525				
Ser																

<210> 82
 <211> 1236
 <212> DNA
 <213> Mouse

<400> 82	
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gcgcgaggac cccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctgggc	120
cgcactgtgc ggctacagt cccagtggag ggggaccac caccgttgac catgtggacc	180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggtctg	240
aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc	300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccaggggaag	360

gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcatcta	gaggctagtg	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgccatcaa	cgccacctac	aaagtggatg	taatccaccc	caaacctcca	720
gggcctccta	tggcttcttc	atcgatcatcc	acaagcctgc	catggcctgt	ggtgatcggc	780
atcccagctg	gtgctgtctt	catcctaggc	actgtgctgc	tctggccttg	ccagaccaag	840
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tcccagagaac	gcagtgggtga	caaggacctg	ccctcattgg	ctgtggggcat	atgtgaggag	960
catggatccg	ccatggcccc	ccagcacatc	ctggcctctg	gctcaactgc	tggccccaag	1020
ctgtacccca	agctatacac	agatgtgcac	acacacacac	atacacacac	ctgcactcac	1080
acgctctcat	gtggagggca	aggttcatca	acaccagcat	gtccactatc	agtgctaaat	1140
acagcgaatc	tccaagcact	gtgtcctgag	gtaggcattt	gggggccaag	gcaacagggt	1200
gggagaattg	agaacaatgg	aggaagagta	tcttag			1236

<210> 83
 <211> 411
 <212> PRT
 <213> Mouse

<400> 83

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20					25					30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
		35					40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50					55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65					70				75						80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
			85					90					95		
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
		100						105					110		
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
	115					120					125				
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
	130					135					140				
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
145					150				155						160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
			165					170					175		
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
	180					185						190			
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
	195					200						205			
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
	210				215						220				
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro	Pro
225					230					235					240
Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro
			245					250					255		
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val
		260					265					270			
Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser

	275		280		285										
Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg
	290					295					300				
Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu
305					310					315				320	
His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr
			325						330					335	
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His
		340						345					350		
Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly
	355					360					365				
Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu
	370					375					380				
Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val
385				390						395				400	
Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser					
			405					410							

<210> 84
 <211> 1305
 <212> DNA
 <213> Mouse

<400> 84

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cgcactgtgc	ggctacagt	cccagtgagg	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccaggggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccagggaag	360
gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	accagccag	ccagcagtgg	420
gagcggactc	gttccaagcc	tgtgttcaca	gggacacacc	ctgtgaacac	aacgggtggc	480
ttcgggtggga	caacgtcctt	ccagtgcagg	gtgcgcagtg	acgtgaagcc	tgtgatccag	540
tggctgaagc	gggtggagta	cggctccgag	ggacgccaca	actccaccat	tgatgtgggt	600
ggccagaagt	ttgtggtgtt	gccacgggt	gatgtgtggt	cacggcctga	tggctcctac	660
ctcaacaagc	tgctcatctc	tcggggccgc	caggatgatg	ctggcatgta	catctgccta	720
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tgtgaggagc	atggatccgc	catggccccc	cagcacatcc	tggcctctgg	ctcaactgct	1080
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tgcactcaca	cgctctcatg	tggagggcaa	ggttcatcaa	caccagcatg	tccactatca	1200
gtgctaaata	cagcgaatct	ccaagcactg	tgtcctgagg	taggcatttg	ggggccaagg	1260
caacaggttg	ggagaattga	gaacaatgga	ggaagagtat	cttag		1305

<210> 85
 <211> 434
 <212> PRT
 <213> Mouse

<400> 85

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5				10				15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
		20					25					30			

<213> Mouse

<400> 86

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cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	cttcacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	420
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acgcatctag	aggctagtga	acacagaaa	aagaagtggg	cactgagctt	gaagaacctg	540
aagcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	600
gccacctaca	aagtggatgt	aatccagcgg	actcgttcca	agcctgtgct	cacagggaca	660
cacctgtga	acacaacggg	ggacttcggg	gggacaacgt	ccttccagtg	caaggtgcgc	720
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cacacacaca	cacatacaca	cacctgcact	cacacgctct	catgtggagg	gcaaggttca	1380
tcaacaccag	catgtccact	atcagtgtga	aatacagcga	atctccaagc	actgtgtcct	1440
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gtatcttag						1509

<210> 87

<211> 502

<212> PRT

<213> Mouse

<400> 87

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
			20					25				30		Val
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35					40					45		Pro
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
	50					55					60			Arg
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65					70				75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
			85					90					95	Lys
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
		100						105					110	Ile
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg
		115					120					125		Val
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala
	130					135						140		Ser
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr
145					150					155				160
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu
														Ser

				165					170					175			
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val		
			180					185					190				
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile		
		195					200					205					
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn		
	210					215					220						
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg		
225					230					235					240		
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly		
			245					250					255				
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe		
			260					265					270				
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr		
		275				280					285						
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met		
	290					295					300						
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala		
305				310					315					320			
Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala		
			325					330						335			
Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile		
			340				345						350				
Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys		
		355				360					365						
Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro		
	370					375					380						
Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp		
385					390				395					400			
Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met		
			405					410					415				
Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu		
		420				425							430				
Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr		
		435				440					445						
Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala		
	450					455					460						
Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro		
465					470				475					480			
Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn		
			485					490					495				
Asn	Gly	Gly	Arg	Val	Ser												
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<210> 88
 <211> 1317
 <212> DNA
 <213> Mouse

<400> 88

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caggaggacc	cagccagcca	gcagtgggca	cggcctcgct	tcacacagcc	ctccaagatg	180
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gggcacccac	ggccagacat	catgtggatg	aaggatgacc	agaccttgac	gcatctagag	300
gctagtgaac	acagaaagaa	gaagtggaca	ctgagcttga	agaacctgaa	gcctgaagac	360
agtggcaagt	acacgtgccg	tgtatctaac	aaggccggtg	ccatcaacgc	cacctacaaa	420

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<210> 89
<211> 438
<212> PRT
<213> Mouse

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<400> 89
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          20          25          30
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
          35          40          45
Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
          50          55          60
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
65          70          75          80
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
          85          90          95
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
          100          105          110
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
          115          120          125
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
          130          135          140
Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
145          150          155          160
Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
          165          170          175
Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
          180          185          190
Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
          195          200          205
Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
          210          215          220
Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met
225          230          235          240
Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
          245          250          255
Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Met Ala
          260          265          270
Ser Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile

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275	280	285
Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu Cys		
290	295	300
Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val Pro		
305	310	315
Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys Asp		
	325	330
Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala Met		
	340	345
Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys Leu		
	355	360
Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His Thr		
370	375	380
Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro Ala		
385	390	395
Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys Pro		
	405	410
Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu Asn		
	420	425
Asn Gly Gly Arg Val Ser		430
435		

<210> 90

<211> 951

<212> DNA

<213> Mouse

<400> 90

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ctatcagtgc	taaatacagc	gaatctccaa	gcactgtgtc	ctgaggtagg	catttggggg	900
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<210> 91

<211> 316

<212> PRT

<213> Mouse

<400> 91

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro	
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Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val	
20	25
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro	

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gatgtgcaca	cacacacaca	tacacacacc	tgcactcaca	cgctctcatg	tgaggaggcaa	1020
gggtcatcaa	caccagcatg	tccactatca	gtgctaaata	cagcgaatct	ccaagcactg	1080
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<210> 93
 <211> 384
 <212> PRT
 <213> Mouse

<400> 93

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			20				25						30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro	
		35					40						45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	
	50					55					60					
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu	
65				70					75						80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys	
			85					90					95			
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile	
		100					105						110			
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	
	115						120					125				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	
	130				135						140					
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	
145				150					155						160	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	
			165					170						175		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	
		180					185						190			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	
	195					200						205				
His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	
	210				215						220					
Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	
225				230					235						240	
Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	
			245					250						255		
Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	
		260					265						270			
Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	
		275				280						285				
Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	
	290				295				300							
Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	
305				310					315						320	
Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	
			325				330							335		
Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	
		340					345					350				
Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	

	355		360		365										
Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser
	370						375				380				

<210> 94
 <211> 1224
 <212> DNA
 <213> Mouse

<400> 94

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cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccaggggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	agcggactcg	ttccaagcct	360
gtgctcacag	ggacacaccc	tgtgaacaca	acggtggact	tcggtgggac	aacgtccttc	420
cagtgcaagg	tgcgcagtga	cgtgaagcct	gtgatccagt	ggctgaagcg	ggtggagtac	480
ggctccgagg	gacgccacaa	ctccaccatt	gatgtgggtg	gccagaagtt	tgtggtgttg	540
cccacgggtg	atgtgtggtc	acggcctgat	ggctcctacc	tcaacaagct	gctcatctct	600
cgggcccgcc	aggatgatgc	tggcatgtac	atctgcctag	gtgcaaatac	catgggctac	660
agtttccgta	gcgccttcct	cactgtatta	ccagacccca	aacctccagg	gcctcctatg	720
gcttcttcat	cgatcatccac	aagcctgcc	tggcctgtgg	tgatcggcat	cccagctggt	780
gctgtcttca	tcctagggac	tgtgctgctc	tggctttgcc	agaccaagaa	gaagccatgt	840
gccccagcat	ctacacttcc	tgtgcctggg	catcgtcccc	cagggacatc	ccgagaacgc	900
agtgggtgaca	aggacctgcc	ctcattggct	gtgggcatat	gtgaggagca	tggatccgcc	960
atggcccccc	agcacatcct	ggcctctggc	tcaactgctg	gccccaaagct	gtaccccaag	1020
ctatacacag	atgtgcacac	acacacacat	acacacacct	gcactcacac	gctctcatgt	1080
ggagggcaag	gttcatcaac	accagcatgt	ccactatcag	tgctaaatac	agcgaatctc	1140
caagcactgt	gtcctgaggt	aggcatttgg	gggccaaggc	aacaggttgg	gagaattgag	1200
aacaatggag	gaagagtatc	ttag				1224

<210> 95
 <211> 407
 <212> PRT
 <213> Mouse

<400> 95

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
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Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20				25						30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
			35				40						45		
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
			50				55						60		
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
					70					75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
					85				90					95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
			100					105					110		
Met	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val
			115				120					125			
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
			130			135					140				
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr

145		150		155		160
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys						
	165		170		175	
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser						
	180		185		190	
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly						
	195		200		205	
Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser						
	210		215		220	
Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Met						
225		230		235		240
Ala Ser Ser Ser Ser Ser Thr Ser Leu Pro Trp Pro Val Val Ile Gly						
	245		250		255	
Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Val Leu Leu Trp Leu						
	260		265		270	
Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val						
	275		280		285	
Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys						
	290		295		300	
Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala						
305		310		315		320
Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys						
	325		330		335	
Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His						
	340		345		350	
Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro						
	355		360		365	
Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys						
	370		375		380	
Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu						
385		390		395		400
Asn Asn Gly Gly Arg Val Ser						
	405					

<210> 96
 <211> 963
 <212> DNA
 <213> Mouse

<400> 96

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caggaggacc	cagccagcca	gcagtgggca	cggcctcgct	tcacacagcc	ctccaagatg	180
aggcgccgag	tgattgcacg	gcctgtgggt	agctctgtgc	ggctcaagtg	tgtggccagt	240
gggcacccac	ggccagacat	catgtggatg	aaggatgacc	agaccttgac	gcatctagag	300
gctagtgaac	acagaaagaa	gaagtggaca	ctgagcttga	agaacctgaa	gcctgaagac	360
agtggcaagt	acacgtgccg	tgtatctaac	aaggccggtg	ccatcaacgc	cacctacaaa	420
gtggatgtaa	tccaccccaa	acctccaggg	cctcctatgg	cttcttcatc	gtcatccaca	480
agcctgccat	ggcctgtggt	gatcggcatc	ccagctgggtg	ctgtcttcat	cctagggcact	540
gtgctgctct	ggctttgcca	gaccaagaag	aagccatgtg	ccccagcatc	tacacttcct	600
gtgcctgggc	atcgtccccc	agggacatcc	cgagaacgca	gtggtgacaa	ggacctgccc	660
tcattggctg	tgggcatatg	tgaggagcat	ggatccgcca	tggcccccca	gcacatcctg	720
gcctctgggt	caactgctgg	ccccaagctg	taccccaagc	tatacacaga	tgtgcacaca	780
cacacacata	cacacacctg	cactcacacg	ctctcatgtg	gagggcaagg	ttcatcaaca	840
ccagcatgtc	cactatcagt	gctaaatata	gcgaatctcc	aagcactgtg	tcctgaggta	900
ggcatttggg	ggccaaggca	acaggttggg	agaattgaga	acaatggagg	aagagtatct	960
tag						963

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<210> 97
<211> 320
<212> PRT
<213> Mouse
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<400> 97

Met 1	Thr	Arg	Ser	Pro 5	Ala	Leu	Leu	Leu	Leu 10	Leu	Leu	Gly	Ala	Leu 15	Pro
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
		35				40						45			
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
	50					55					60				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
65					70					75					80
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
				85				90						95	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
			100					105					110		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
		115				120						125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
	130					135					140				
His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr
145					150					155					160
Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe
				165				170						175	
Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro
		180					185					190			
Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly
		195				200						205			
Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val
	210					215					220				
Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu
225					230					235					240
Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr
				245				250						255	
Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser
			260				265						270		
Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu
		275					280					285			
Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly
	290					295					300				
Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser
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<210> 98
<211> 1032
<212> DNA
<213> Mouse
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<400> 98

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caggaggacc  cagccagcca  gcagtgggag  cggaactcgtt  ccaagcctgt  gctcacaggg     180
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acacaccctg	tgaacacaac	ggtggacttc	ggtggggacaa	cgtccttcca	gtgcaagggtg	240
cgcagtgaacg	tgaagcctgt	gatccagtgg	ctgaagcggg	tggagtacgg	ctccgaggga	300
cgccacaact	ccaccattga	tgtgggtggc	cagaagtttg	tgggtgttgcc	cacgggtgat	360
gtgtgggtcac	ggcctgatgg	ctcctacctc	aacaagctgc	tcattctctcg	ggcccgccag	420
gatgatgctg	gcatgtacat	ctgcctaggt	gcaaatacca	tgggctacag	tttccgtagc	480
gccttcctca	ctgtattacc	agaccccaaa	cctccagggc	ctcctatggc	ttcttcatcg	540
tcatccacaa	gcctgccatg	gcctgtggtg	atcggcatcc	cagctggtgc	tgtcttcatc	600
ctaggcactg	tgctgctctg	gctttgccag	accaagaaga	agccatgtgc	cccagcatct	660
acacttcctg	tgctgggca	tcgtcccca	gggacatccc	gagaacgcag	tggtgacaag	720
gacctgccct	cattggctgt	gggcatatgt	gaggagcatg	gatccgccat	ggccccccag	780
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cctgaggtag	gcatttgggg	gccaaggcaa	caggttggga	gaattgagaa	caatggagga	1020
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<210> 99

<211> 343

<212> PRT

<213> Mouse

<400> 99

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
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Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
		35					40					45			
Trp	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val
	50					55					60				
Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
65					70					75					80
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr
				85				90					95		
Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys
			100					105					110		
Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser
		115					120				125				
Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly
	130					135					140				
Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser
145				150						155					160
Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met
				165					170					175	
Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly
			180					185					190		
Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu
		195					200					205			
Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val
	210					215					220				
Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys
225					230					235					240
Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala
				245				250					255		
Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys
			260					265					270		
Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His

	275					280						285					
Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro		
	290					295					300						
Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys		
305					310					315					320		
Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu		
				325					330					335			
Asn	Asn	Gly	Gly	Arg	Val	Ser											
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<210> 100
 <211> 1236
 <212> DNA
 <213> Mouse

<400> 100

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cctgtgggta	gctctgtgcg	gctcaagtgt	gtggccagtg	ggcacccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgacg	catctagagg	ctagtgaaca	cagaaagaag	240
aagtggacac	tgagcttgaa	gaacctgaag	cctgaagaca	gtggcaagta	cacgtgccgt	300
gtatctaaca	aggccggtgc	catcaacgcc	acctacaaag	tggatgtaat	ccagcggact	360
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acaacgtcct	tccagtgcaa	ggtgcgcagt	gacgtgaagc	ctgtgatcca	gtggctgaag	480
cgggtggagt	acggctccga	gggacgccac	aactccacca	ttgatgtggg	tggccagaag	540
tttgtggtgt	tgcccacggg	tgatgtgtgg	tcacggcctg	atggctccta	cctcaacaag	600
ctgctcatct	ctcgggcccc	ccaggatgat	gctggcatgt	acatctgcct	aggtgcaa	660
accatgggct	acagtttccg	tagcgccttc	ctcactgtat	taccagaccc	caaacctcca	720
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tcccgagaac	gcagtgggtga	caaggacctg	ccctcattgg	ctgtgggcat	atgtgaggag	960
catggatccg	ccatggcccc	ccagcacatc	ctggcctctg	gctcaactgc	tggccccaag	1020
ctgtacccca	agctatacac	agatgtgcac	acacacacac	atacacacac	ctgcactcac	1080
acgctctcat	gtggagggca	aggttcatca	acaccagcat	gtccactatc	agtgctaaat	1140
acagcgaatc	tccaagcact	gtgtcctgag	gtaggcattt	gggggccaag	gcaacagggt	1200
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<210> 101
 <211> 411
 <212> PRT
 <213> Mouse

<400> 101

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Ser	Ala	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Lys
			20				25					30		
Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg
		35					40					45		Leu
Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met
	50					55					60			Lys
Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys
65					70				75					80
Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly
				85					90					95
Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr

			100					105					110				
Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly		
		115					120					125					
Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe		
	130					135					140						
Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys		
145					150					155					160		
Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val		
				165				170						175			
Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg		
		180					185					190					
Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln		
	195					200						205					
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr		
	210			215						220							
Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	Pro	Pro		
225				230				235							240		
Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro			
			245			250						255					
Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val		
		260				265						270					
Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser		
	275				280					285							
Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg		
	290				295					300							
Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu		
305				310					315						320		
His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr		
			325				330							335			
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His		
		340				345						350					
Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly		
	355				360							365					
Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu		
	370				375					380							
Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val		
385				390						395					400		
Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser							
			405			410											

<210> 102
 <211> 870
 <212> DNA
 <213> Mouse

<400> 102																	
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cgcactgtgc	ggctacagtg	cccagtggag	ggggaccac	caccgttgac	catgtggacc											180	
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccaggggtctg											240	
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc											300	
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	accccaaacc	tccagggcct											360	
cctatggctt	cttcatcgtc	atccacaagc	ctgccatggc	ctgtgggtgat	cggcatccca											420	
gctggtgctg	tcttcatcct	aggcactgtg	ctgctctggc	tttgccagac	caagaagaag											480	
ccatgtgccc	cagcatctac	acttcctgtg	cctggggcatc	gtcccccagg	gacatcccga											540	
gaacgcagtg	gtgacaagga	cctgccctca	ttggctgtgg	gcatatgtga	ggagcatgga											600	
tccgccatgg	ccccccagca	catcctggcc	tctgggtcaa	ctgctggccc	caagctgtac											660	

cccaagctat acacagatgt gcacacacac acacatacac acacctgcac tcacacgctc	720
tcattgtggag ggcaagggttc atcaacacca gcatgtccac tatcagtgtc aaatacagcg	780
aattctccaag cactgtgtcc tgaggtaggc atttgggggc caaggcaaca ggttgggaga	840
attgagaaca atggaggaag agtatcttag	870

<210> 103
 <211> 289
 <212> PRT
 <213> Mouse

<400> 103

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro	
1				5				10					15			
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val	
			20				25						30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro	
		35					40					45				
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg	
	50					55					60					
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu	
65				70				75							80	
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys	
			85					90					95			
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile	
			100					105					110			
Met	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	
		115				120						125				
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	
	130					135					140					
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	
145				150				155							160	
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	
			165					170					175			
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	
			180					185					190			
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	
	195						200					205				
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	
	210					215					220					
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	
225				230						235					240	
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	
			245					250					255			
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	
		260						265					270			
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	
		275					280					285				

Ser

<210> 104
 <211> 678
 <212> DNA
 <213> Mouse

<400> 104

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caggaggacc	cagccagcca	gcagtgggac	cccaaacctc	cagggcctcc	tatggcttct	180
tcacgtcat	ccacaagcct	gccatggcct	gtggtgatcg	gcatcccagc	tggtgctgtc	240
ttcatcctag	gcactgtgct	gctctggctt	tgccagacca	agaagaagcc	atgtgccc	300
gcatctacac	ttcctgtgcc	tgggcatcgt	ccccagga	catcccagaga	acgcagtgg	360
gacaaggacc	tgccctcatt	ggctgtgggc	atatgtgagg	agcatggatc	cgccatggcc	420
ccccagcaca	tcctggcctc	tggtcaact	gctggcccca	agctgtaccc	caagctatac	480
acagatgtgc	acacacacac	acatacacac	acctgcactc	acacgctctc	atgtggaggg	540
caaggttcat	caacaccagc	atgtccacta	tcagtgctaa	atacagcgaa	tctccaagca	600
ctgtgtcctg	aggtaggcat	ttggggggcca	aggcaacagg	ttgggagaat	tgagaacaat	660
ggaggaagag	tatcttag					678

<210> 105
 <211> 225
 <212> PRT
 <213> Mouse

<400> 105

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5				10						15	
Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
		35					40					45			
Trp	Asp	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser
	50					55					60				
Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val
65					70				75						80
Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys
				85				90					95		
Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro
			100					105					110		
Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala
		115					120					125			
Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile
	130					135					140				
Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr
145					150				155						160
Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu
				165				170						175	
Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val
			180				185						190		
Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp
	195					200						205			
Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val
	210					215					220				

Ser
225

<210> 106
 <211> 882
 <212> DNA
 <213> Mouse

<400> 106

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgagcac	ggcctcgctt	cacacagccc	tccaagatga	ggcgccgagt	gattgcacgg	120

cctgtgggta	gctctgtgcg	gctcaagtgt	gtggccagt	ggcaccacg	gccagacatc	180
atgtggatga	aggatgacca	gaccttgacg	catctagagg	ctagtgaaca	cagaaagaag	240
aagtggacac	tgagcttgaa	gaacctgaag	cctgaagaca	gtggcaagta	cacgtgccgt	300
gtatctaaca	aggccggtgc	catcaacgcc	acctacaaag	tggatgtaat	ccaccccaaa	360
cctccagggc	ctcctatggc	ttcttcatcg	tcatccacaa	gcctgccatg	gcctgtggtg	420
atcggcaccc	cagctggtgc	tgtcttcatc	ctaggcactg	tgctgctctg	gctttgccag	480
accaagaaga	agccatgtgc	cccagcatct	acacttcctg	tgcttgggca	tcgtcccca	540
gggacatccc	gagaacgcag	tggtgacaag	gacctgccct	cattggctgt	gggcatatgt	600
gaggagcatg	gatccgccat	ggccccccag	cacatcctgg	cctctggctc	aactgctggc	660
cccaagctgt	acccaagct	atacacagat	gtgcacacac	acacacatac	acacacctgc	720
actcacacgc	tctcatgtgg	agggcaaggt	tcatcaacac	cagcatgtcc	actatcagtg	780
ctaaatacag	cgaatctcca	agcactgtgt	cctgaggtag	gcatttgggg	gccaaggcaa	840
caggttggga	gaattgagaa	caatggagga	agagtatctt	ag		882

<210> 107

<211> 293

<212> PRT

<213> Mouse

<400> 107

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5				10					15	
Ser	Ala	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Lys
			20					25				30		
Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg
		35					40					45		Leu
Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Lys
	50					55					60			
Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys
65					70				75					80
Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly
				85					90					95
Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr
			100					105					110	Tyr
Lys	Val	Asp	Val	Ile	His	Pro	Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala
		115					120					125		Ser
Ser	Ser	Ser	Ser	Thr	Ser	Leu	Pro	Trp	Pro	Val	Val	Ile	Gly	Ile
		130				135					140			Pro
Ala	Gly	Ala	Val	Phe	Ile	Leu	Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys
145					150				155					Gln
Thr	Lys	Lys	Lys	Pro	Cys	Ala	Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro
				165				170						Gly
His	Arg	Pro	Pro	Gly	Thr	Ser	Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp
			180					185					190	Leu
Pro	Ser	Leu	Ala	Val	Gly	Ile	Cys	Glu	Glu	His	Gly	Ser	Ala	Met
		195					200					205		Ala
Pro	Gln	His	Ile	Leu	Ala	Ser	Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu
		210				215					220			Tyr
Pro	Lys	Leu	Tyr	Thr	Asp	Val	His	Thr	His	Thr	His	Thr	His	Thr
225					230				235					Cys
Thr	His	Thr	Leu	Ser	Cys	Gly	Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala
				245					250					Cys
Pro	Leu	Ser	Val	Leu	Asn	Thr	Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro
			260					265					270	Glu
Val	Gly	Ile	Trp	Gly	Pro	Arg	Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn
		275					280					285		Asn
Gly	Gly	Arg	Val	Ser										

290

<210> 108
<211> 951
<212> DNA
<213> Mouse

<400> 108
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
gcgcgagagc ggactcggtc caagcctgtg ctcacaggga cacaccctgt gaacacaacg 120
gtggacttcg gtgggacaac gtccttccag tgcaagggtg gcagtgcgtg gaagcctgtg 180
atccagtggc tgaagcgggt ggagtacggc tccgaggggac gccacaactc caccattgat 240
gtgggtggcc agaagtttgt ggtgttgccc acgggtgatg tgtgggtcacg gcctgatggc 300
tcctacctca acaagctgct catctctcgg gcccgccagg atgatgctgg catgtacatc 360
tgcctagggtg caaataccat gggctacagt ttccgtagcg ccttcctcac tgtattacca 420
gaccccaaac ctccagggcc tcctatggct tcttcatcgt catccacaag cctgccatgg 480
cctgtggtga tcggcatccc agctggtgct gtcttcatcc taggcactgt gctgctctgg 540
ctttgccaga ccaagaagaa gccatgtgcc ccagcatcta cacttcctgt gcctgggcat 600
cgtccccccag ggacatcccc agaacgcagt ggtgacaagg acctgccctc attggctgtg 660
ggcatatgtg aggagcatgg atccgccatg gccccccagc acatcctggc ctctgggtca 720
actgctggcc ccaagctgta cccaagcta tacacagatg tgcacacaca cacacataca 780
cacacctgca ctcacacgct ctcagtgtga gggcaagggt catcaacacc agcatgtcca 840
ctatcagtgc taaatacagc gaatctccaa gcactgtgtc ctgaggtagg catttggggg 900
ccaaggcaac aggttgggag aattgagaac aatggaggaa gagtatctta g 951

<210> 109
<211> 316
<212> PRT
<213> Mouse

<400> 109
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15
Ser Ala Glu Ala Ala Arg Glu Arg Thr Arg Ser Lys Pro Val Leu Thr
20 25 30
Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser
35 40 45
Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu
50 55 60
Lys Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp
65 70 75 80
Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser
85 90 95
Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg
100 105 110
Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly
115 120 125
Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys Pro
130 135 140
Pro Gly Pro Pro Met Ala Ser Ser Ser Ser Ser Thr Ser Leu Pro Trp
145 150 155 160
Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu Gly Thr
165 170 175
Val Leu Leu Trp Leu Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala
180 185 190
Ser Thr Leu Pro Val Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu

	195		200		205
Arg	Ser Gly Asp Lys Asp Leu	Pro Ser Leu Ala	Val Gly Ile Cys Glu		
	210	215	220		
Glu	His Gly Ser Ala Met Ala	Pro Gln His Ile	Leu Ala Ser Gly Ser		
225		230	235		240
Thr	Ala Gly Pro Lys Leu Tyr	Pro Lys Leu Tyr	Thr Asp Val His Thr		
	245	250	255		
His	Thr His Thr His Thr Cys	Thr His Thr Leu Ser	Cys Gly Gly Gln		
	260	265	270		
Gly	Ser Ser Thr Pro Ala Cys	Pro Leu Ser Val	Leu Asn Thr Ala Asn		
	275	280	285		
Leu	Gln Ala Leu Cys Pro Glu	Val Gly Ile Trp	Gly Pro Arg Gln Gln		
	290	295	300		
Val	Gly Arg Ile Glu Asn Asn	Gly Gly Arg Val	Ser		
305		310	315		

<210> 110
 <211> 597
 <212> DNA
 <213> Mouse

<400> 110

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gcgcgagacc	ccaaacctcc	agggcctcct	atggcttctt	catcgtcatc	cacaagcctg	120
ccatggcctg	tggtgatcgg	catcccagct	ggtgctgtct	tcctcctagg	cactgtgctg	180
ctctggcttt	gccagaccaa	gaagaagcca	tgtgccccag	catctacact	tcctgtgcct	240
gggcatcgtc	ccccagggac	atcccagaaa	cgcagtgggtg	acaaggacct	gccctcattg	300
gctgtgggca	tatgtgagga	gcatggatcc	gccatggccc	cccagcacat	cctggcctct	360
ggctcaactg	ctggccccaa	gctgtacccc	aagctataca	cagatgtgca	cacacacaca	420
catacacaca	cctgcactca	cacgctctca	tgtggagggc	aaggttcac	aacaccagca	480
tgtccactat	cagtgcataa	tacagcgaat	ctccaagcac	tgtgtcctga	ggtaggcatt	540
tggggggccaa	ggcaacaggt	tgggagaatt	gagaacaatg	gaggaagagt	atcttag	597

<210> 111
 <211> 198
 <212> PRT

<213> Mouse

<400> 111

Met	Thr Arg Ser Pro Ala	Leu Leu Leu Leu Leu	Gly Ala Leu Pro		
1	5	10	15		
Ser	Ala Glu Ala Ala Arg	Asp Pro Lys Pro Pro	Gly Pro Pro Met Ala		
	20	25	30		
Ser	Ser Ser Ser Ser Thr	Ser Leu Pro Trp Pro	Val Val Ile Gly Ile		
	35	40	45		
Pro	Ala Gly Ala Val Phe	Ile Leu Gly Thr Val	Leu Leu Trp Leu Cys		
	50	55	60		
Gln	Thr Lys Lys Lys Pro	Cys Ala Pro Ala Ser	Thr Leu Pro Val Pro		
65	70	75	80		
Gly	His Arg Pro Pro Gly	Thr Ser Arg Glu Arg	Ser Gly Asp Lys Asp		
	85	90	95		
Leu	Pro Ser Leu Ala Val	Gly Ile Cys Glu Glu	His Gly Ser Ala Met		
	100	105	110		
Ala	Pro Gln His Ile Leu	Ala Ser Gly Ser Thr	Ala Gly Pro Lys Leu		
	115	120	125		
Tyr	Pro Lys Leu Tyr Thr	Asp Val His Thr His	Thr His Thr His Thr		

130		135		140
Cys Thr His Thr Leu Ser	Cys Gly Gly Gln Gly	Ser Ser Thr Pro Ala		
145	150	155	160	
Cys Pro Leu Ser Val Leu	Asn Thr Ala Asn Leu	Gln Ala Leu Cys Pro		
	165	170	175	
Glu Val Gly Ile Trp Gly	Pro Arg Gln Gln Val	Gly Arg Ile Glu Asn		
	180	185	190	
Asn Gly Gly Arg Val Ser				
195				

<210> 112
 <211> 1060
 <212> DNA
 <213> Mouse

<400> 112

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gcgcgaggac	cccccaagaat	ggcagacaaa	gtggtcccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtgagg	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggggaag	360
gagagccctg	ggccagggtg	ttcttcgggg	ggccaggagg	acccagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcatcta	gaggctagt	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgccatcaa	cgccacctac	aaagtggatg	taatccagcg	gactcgttcc	720
aagcctgtgc	tcacagggac	acaccctgtg	aacacaacgg	tggacttcgg	tgggacaacg	780
tccttccagt	gcaaggtgcg	cagtgcgctg	aagcctgtga	tccagtggct	gaagcgggtg	840
gagtacggct	ccgagggacg	ccacaactcc	accattgatg	tgggtggcca	gaagtttgtg	900
gtgttgccca	cgggtgatgt	gtggtcacgg	cctgatggct	cctacctcaa	caagctgctc	960
atctctcggg	cccgccagga	tgatgctggc	atgtacatct	gcctaggtgc	aaataccatg	1020
ggctacagtt	tccgtagcgc	cttcctcact	gtattaccag			1060

<210> 113
 <211> 353
 <212> PRT
 <213> Mouse

<400> 113

Met Thr Arg Ser Pro Ala	Leu Leu Leu Leu Leu	Gly Ala Leu Pro
1	5	10
Ser Ala Glu Ala Ala Arg	Gly Pro Pro Arg Met	Ala Asp Lys Val Val
20	25	30
Pro Arg Gln Val Ala Arg	Leu Gly Arg Thr Val	Arg Leu Gln Cys Pro
35	40	45
Val Glu Gly Asp Pro Pro	Pro Leu Thr Met Trp	Thr Lys Asp Gly Arg
50	55	60
Thr Ile His Ser Gly Trp	Ser Arg Phe Arg Val	Leu Pro Gln Gly Leu
65	70	75
Lys Val Lys Glu Val Glu	Ala Glu Asp Ala Gly	Val Tyr Val Cys Lys
85	90	95
Ala Thr Asn Gly Phe Gly	Ser Leu Ser Val Asn	Tyr Thr Leu Ile Ile
100	105	110
Met Asp Asp Ile Ser Pro	Gly Lys Glu Ser Pro	Gly Pro Gly Gly Ser
115	120	125

Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
130						135					140				
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
145					150					155					160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
				165					170					175	
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
			180					185					190		
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
	195						200					205			
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
	210					215					220				
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser
225					230					235					240
Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe
				245					250					255	
Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro
			260					265					270		
Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His
	275						280					285			
Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr
	290					295					300				
Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu
305					310					315					320
Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly
				325					330					335	
Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu
			340					345					350		

Pro

<210> 114
 <211> 706
 <212> DNA
 <213> Mouse

<400> 114

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gcgcgaggac	ccccagaat	ggcagacaaa	gtggtccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagt	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggaag	360
gagagccctg	ggccaggtgg	ttcttcgggg	ggccaggagg	accagccag	ccagcagtgg	420
gcacggcctc	gcttcacaca	gccctccaag	atgaggcgcc	gagtgattgc	acggcctgtg	480
ggtagctctg	tgcggctcaa	gtgtgtggcc	agtgggcacc	cacggccaga	catcatgtgg	540
atgaaggatg	accagacctt	gacgcactta	gaggctagt	aacacagaaa	gaagaagtgg	600
acactgagct	tgaagaacct	gaagcctgaa	gacagtggca	agtacacgtg	ccgtgtatct	660
aacaaggccg	gtgccatcaa	cgccacctac	aaagtggatg	taatcc		706

<210> 115
 <211> 235
 <212> PRT
 <213> Mouse

<400> 115

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro

1	5	10	15												
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
	20		25		30										
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
	35		40		45										
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50		55		60										
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65			70		75										80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
			85		90										
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
			100		105										
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
	115		120		125										
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Ala	Arg	Pro	Arg
	130		135		140										
Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val	Ile	Ala	Arg	Pro	Val
145			150		155										160
Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser	Gly	His	Pro	Arg	Pro
			165		170										175
Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala
			180		185										190
Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys
	195		200		205										
Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly
	210		215		220										
Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile					
225			230		235										

<210> 116
 <211> 775
 <212> DNA
 <213> Mouse

<400> 116

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	cccgaagaat	ggcagacaaa	gtgggtccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	atgatattag	tccaggggaag	360
gagagccctg	ggccagggtg	ttcttcgggg	ggccaggagg	accagccag	ccagcagtgg	420
gagcggactc	gttccaagcc	tgtgctcaca	gggacacacc	ctgtgaacac	aacggtggac	480
ttcgggtggga	caacgtcctt	ccagtgcgaag	gtgcgcagtg	acgtgaagcc	tgtgatccag	540
tggctgaagc	gggtggagta	cggctccgag	ggacgccaca	actccaccat	tgatgtgggt	600
ggccagaagt	ttgtgggtgtt	gcccacgggt	gatgtgtggt	cacggcctga	tggctcctac	660
ctcaacaagc	tgctcatctc	tcgggcccgc	caggatgatg	ctggcatgta	catctgccta	720
ggtgcaaata	ccatgggcta	cagtttccgt	agcgccttcc	tactgtatt	accag	775

<210> 117
 <211> 258
 <212> PRT
 <213> Mouse

<400> 117

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5				10						15	
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
		20					25					30			
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
	35					40					45				
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50					55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65				70					75						80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
			85			90						95			
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
		100				105						110			
Met	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro	Gly	Pro	Gly	Gly	Ser
	115					120					125				
Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln	Trp	Glu	Arg	Thr	Arg
	130					135					140				
Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp
145				150					155						160
Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys
			165			170							175		
Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg
		180				185						190			
His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro
	195					200					205				
Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu
	210					215					220				
Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu
225				230					235						240
Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val
			245						250				255		

Leu Pro

<210> 118
 <211> 979
 <212> DNA
 <213> Mouse

<400> 118

atgacgcgga	gccccgcgct	gctgctgctg	ctattggggg	ccctcccgtc	ggctgaggcg	60
gcgcgaggac	ccccagaat	ggcagacaaa	gtgggtccac	ggcaggtggc	ccgcctgggc	120
cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccagggctctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatcatgg	cacggcctcg	cttcacacag	360
ccctccaaga	tgaggcgccg	agtgattgca	cggcctgtgg	gtagctctgt	gcggctcaag	420
tgtgtggcca	gtgggcaccc	acggccagac	atcatgtgga	tgaaggatga	ccagaccttg	480
acgcatctag	aggctagtga	acacagaaaag	aagaagtgga	cactgagctt	gaagaacctg	540
aagcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	600
gccacctaca	aagtggatgt	aatccagcgg	actcgttcca	agcctgtgct	cacagggaca	660
caccctgtga	acacaacggt	ggacttcggt	gggacaacgt	ccttccagtg	caaggtgcgc	720
agtgacgtga	agcctgtgat	ccagtggctg	aagcgggtgg	agtacggctc	cgagggacgc	780
cacaactcca	ccattgatgt	gggtggccag	aagtttgtgg	tgttgccac	gggtgatgtg	840
tggtcacggc	ctgatggctc	ctacctcaac	aagctgctca	tctctcgggc	ccgccaggat	900

gatgctggca tgtacatctg cctaggtgca aataccatgg gctacagttt ccgtagcgcc
 ttcctcactg tattaccag

960
 979

<210> 119
 <211> 326
 <212> PRT
 <213> Mouse

<400> 119

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5						10				15	
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val	Val
			20				25						30		
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys	Pro
		35					40					45			
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly	Arg
	50					55					60				
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly	Leu
65					70					75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys	Lys
				85					90					95	
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile	Ile
			100					105					110		
Met	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
		115					120					125			
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
	130					135					140				
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
145					150					155					160
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
				165					170					175	
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
		180					185						190		
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
	195						200					205			
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
	210					215					220				
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
225					230					235					240
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly
				245					250					255	
Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe
			260					265					270		
Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr
		275					280					285			
Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met
	290					295					300				
Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala
305					310					315					320
Phe	Leu	Thr	Val	Leu	Pro										
				325											

<210> 120
 <211> 787
 <212> DNA
 <213> Mouse

```

<400> 120
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg      60
gcgcgagatg atattagtcc aggggaaggag agccctgggc caggtgggtc ttcggggggc      120
caggaggacc cagccagcca gcagtgggca cggcctcgct tcacacagcc ctccaagatg      180
aggcgccgag tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tgtggccagt      240
gggcacccac ggccagacat catgtggatg aaggatgacc agaccttgac gcatctagag      300
gctagtgaac acagaaagaa gaagtggaca ctgagcttga agaacctgaa gcctgaagac      360
agtggcaagt acacgtgccg tgtatctaac aaggccggtg ccatcaacgc cacctacaaa      420
gtggatgtaa tccagcggac tcgttccaag cctgtgctca cagggaacaca ccctgtgaac      480
acaacggtgg acttcggtgg gacaacgtcc ttccagtgc aagtgcgag tgacgtgaag      540
cctgtgatcc agtggctgaa gcgggtggag tacggctccg agggacgcca caactccacc      600
attgatgtgg gtggccagaa gtttgtggtg ttgccacgg gtgatgtgtg gtcacggcct      660
gatggctcct acctcaacaa gctgctcatc tctcggggcc gccaggatga tgctggcatg      720
tacatctgcc taggtgcaaa taccatgggc tacagtttcc gtagcgcctt cctcactgta      780
ttaccag                                         787

```

```

<210> 121
<211> 262
<212> PRT
<213> Mouse

```

```

<400> 121
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1          5          10          15
Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro
          20          25          30
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
          35          40          45
Trp Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
          50          55          60
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
65          70          75          80
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
          85          90          95
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
          100          105          110
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
          115          120          125
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
          130          135          140
Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn
145          150          155          160
Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val Arg
          165          170          175
Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr Gly
          180          185          190
Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
          195          200          205
Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
          210          215          220
Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly Met
225          230          235          240
Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
          245          250          255
Phe Leu Thr Val Leu Pro
          260

```

<210> 122
 <211> 421
 <212> DNA
 <213> Mouse

<400> 122
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctgggc 120
 cgcactgtgc ggctacagtg cccagtggag ggggacccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctctg 240
 aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg atgatattag tccaggggaag 360
 gagagccctg ggccaggtgg ttcttcgggg ggccaggagg acccagccag ccagcagtgg 420
 g 421

<210> 123
 <211> 140
 <212> PRT
 <213> Mouse

<400> 123
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro Gly Pro Gly Gly Ser
 115 120 125
 Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln Trp
 130 135 140

<210> 124
 <211> 625
 <212> DNA
 <213> Mouse

<400> 124
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctgggc 120
 cgcactgtgc ggctacagtg cccagtggag ggggacccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctctg 240
 aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg cagggcctcg cttcacacag 360
 ccctccaaga tgaggcgccg agtgattgca cggcctgtgg gtagctctgt gcggctcaag 420
 tgtgtggcca gtgggcaccc acggccagac atcatgtgga tgaaggatga ccagaccttg 480
 acgcatctag aggctagtga acacagaaag aagaagtgga cactgagctt gaagaacctg 540
 aagcctgaag acagtggcaa gtacacgtgc cgtgtatcta acaaggccgg tgccatcaac 600

gccacctaca aagtggatgt aatcc

625

<210> 125
<211> 208
<212> PRT
<213> Mouse

<400> 125
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
1 5 10 15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
20 25 30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
35 40 45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
50 55 60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65 70 75 80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
85 90 95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
100 105 110
Met Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys Met Arg Arg Arg Val
115 120 125
Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu Lys Cys Val Ala Ser
130 135 140
Gly His Pro Arg Pro Asp Ile Met Trp Met Lys Asp Asp Gln Thr Leu
145 150 155 160
Thr His Leu Glu Ala Ser Glu His Arg Lys Lys Lys Trp Thr Leu Ser
165 170 175
Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val
180 185 190
Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile
195 200 205

<210> 126
<211> 694
<212> DNA
<213> Mouse

<400> 126
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
gcgcgaggac ccccaagaat ggcagacaaa gtggtccac ggcaggtggc ccgcctgggc 120
cgactgtgc ggctacagtg cccagtggag ggggaccac caccgttgac catgtggacc 180
aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccagggctctg 240
aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
tttggcagcc tcagcgtcaa ctacactctc atcatcatgg agcggactcg ttccaagcct 360
gtgctcacag ggacacaccc tgtgaacaca acggtggact tcggtgggac aacgtccttc 420
cagtgaagg tgcgcagtga cgtgaagcct gtgatccagt ggctgaagcg ggtggagtac 480
ggctccgagg gacgccacaa ctccaccatt gatgtgggtg gccagaagtt tgtgggtgttg 540
cccacgggtg atgtgtggtc acggcctgat ggctcctacc tcaacaagct gctcatctct 600
cgggcccgcc aggatgatgc tggcatgtac atctgcctag gtgcaaatac catgggctac 660
agtttccgta gcgccttcct cactgtatta ccag 694

<210> 127
<211> 231
<212> PRT

<213> Mouse

<400> 127

```
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1          5          10          15
Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
          20          25          30
Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
          35          40          45
Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
          50          55          60
Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
65          70          75          80
Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
          85          90          95
Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
          100          105          110
Met Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val
          115          120          125
Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val
          130          135          140
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr
145          150          155          160
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys
          165          170          175
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser
          180          185          190
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly
          195          200          205
Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser
          210          215          220
Ala Phe Leu Thr Val Leu Pro
225          230
```

<210> 128

<211> 433

<212> DNA

<213> Mouse

<400> 128

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atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg      60
gcgcgagatg atattagtcc agggaaggag agccctgggc caggtgggtc ttcggggggc      120
caggaggacc cagccagcca gcagtgggca cggcctcgct tcacacagcc ctccaagatg      180
aggcgccgag tgattgcacg gcctgtgggt agctctgtgc ggctcaagtg tgtggccagt      240
gggcacccac ggccagacat catgtggatg aaggatgacc agacctgac gcatctagag      300
gctagtgaac acagaaagaa gaagtggaca ctgagcttga agaacctgaa gcctgaagac      360
agtggcaagt acacgtgccg tgtatctaac aaggccggtg ccatcaacgc cacctacaaa      420
gtggatgtaa tcc                                     433
```

<210> 129

<211> 144

<212> PRT

<213> Mouse

<400> 129

```
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1          5          10          15
```

Ser	Ala	Glu	Ala	Ala	Arg	Asp	Asp	Ile	Ser	Pro	Gly	Lys	Glu	Ser	Pro
			20					25					30		
Gly	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
		35					40					45			
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
	50					55					60				
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
65					70					75					80
Gly	His	Pro	Arg	Pro	Asp	Ile	Met	Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu
				85					90					95	
Thr	His	Leu	Glu	Ala	Ser	Glu	His	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
			100					105					110		
Leu	Lys	Asn	Leu	Lys	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
		115					120					125			
Ser	Asn	Lys	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
	130					135					140				

<210> 130
 <211> 502
 <212> DNA
 <213> Mouse

<400> 130	
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg	60
gcgcgagatg atattagtcc agggaaggag agccctgggc caggtgggtc ttcggggggc	120
caggaggacc cagccagcca gcagtgggag cggactcggt ccaagcctgt gctcacaggg	180
acacaccctg tgaacacaac ggtggacttc ggtgggacaa cgtccttcca gtgcaagggtg	240
cgcagtgcg tgaagcctgt gatccagtgg ctgaagcggg tggagtacgg ctccgaggga	300
cgccacaact ccaccattga tgtgggtggc cagaagtttg tgggtgttgcc cacgggtgat	360
gtgtggtcac ggcctgatgg ctccctacctc aacaagctgc tcatctctcg ggcccgccag	420
gatgatgctg gcatgtacat ctgcctaggt gcaaatacca tgggctacag tttccgtagc	480
gccttcctca ctgtattacc ag	502

<210> 131
 <211> 167
 <212> PRT
 <213> Mouse

<400> 131	
Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro	
1	15
Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro	
	30
Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln	
	45
Trp Glu Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val	
50	60
Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val	
65	80
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu Tyr	
	95
Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys	
	110
Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser	
	125
Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln Asp Asp Ala Gly	
130	140

Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser
 145 150 155 160
 Ala Phe Leu Thr Val Leu Pro
 165

<210> 132
 <211> 706
 <212> DNA
 <213> Mouse

<400> 132
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgagcac ggctcgcctt cacacagccc tccaagatga ggcgccgagt gattgcacgg 120
 cctgtgggta gctctgtgcg gctcaagtgt gtggccagtg ggcacccacg gccagacatc 180
 atgtggatga aggatgacca gaccttgacg catctagagg ctagtgaaca cagaaagaag 240
 aagtggacac tgagcttgaa gaacctgaag cctgaagaca gtggcaagta cacgtgccgt 300
 gtatctaaca aggccggtgc catcaacgcc acctacaaag tggatgtaat ccagcggact 360
 cgttccaagc ctgtgctcac agggacacac cctgtgaaca caacggtgga cttcggtggg 420
 acaacgtcct tccagtgcaa ggtgcgcagt gacgtgaagc ctgtgatcca gtggctgaag 480

 cgggtggagt acggctccga gggacgccac aactccacca ttgatgtggg tggccagaag 540
 tttgtggtgt tgcccacggg tgatgtgtgg tcacggcctg atggctccta cctcaacaag 600
 ctgctcatct ctcgggcccc ccaggatgat gctggcatgt acatctgcct aggtgcaaat 660
 accatgggct acagtttccg tagcgccttc ctactgtat taccag 706

<210> 133
 <211> 235
 <212> PRT
 <213> Mouse

<400> 133
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys
 20 25 30
 Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu
 35 40 45
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys
 50 55 60
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys
 65 70 75 80
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys
 85 90 95
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr
 100 105 110
 Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val Leu Thr Gly
 115 120 125
 Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe
 130 135 140
 Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys
 145 150 155 160
 Arg Val Glu Tyr Gly Ser Glu Gly Arg His Asn Ser Thr Ile Asp Val
 165 170 175
 Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg
 180 185 190
 Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Ser Arg Ala Arg Gln
 195 200 205

Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr
 210 215 220
 Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro
 225 230 235

<210> 134
 <211> 340
 <212> DNA
 <213> Mouse

<400> 134
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgaggac cccaagaat ggcagacaaa gtgggtccac ggcaggtggc ccgcctgggc 120
 cgcaactgtgc ggctacagtg cccagtggag ggggacccac caccgttgac catgtggacc 180
 aaagatggcc gcacaatcca cagtggctgg agccgcttcc gtgtgctgcc ccaggggtctg 240
 aaggtgaagg aggtggaggc cgaggatgcc ggtgtttatg tgtgcaaggc caccaatggc 300
 tttggcagcc tcagcgtcaa ctacactctc atcatcatgg 340

<210> 135
 <211> 113
 <212> PRT
 <213> Mouse

<400> 135
 Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Gly Pro Pro Arg Met Ala Asp Lys Val Val
 20 25 30
 Pro Arg Gln Val Ala Arg Leu Gly Arg Thr Val Arg Leu Gln Cys Pro
 35 40 45
 Val Glu Gly Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg
 50 55 60
 Thr Ile His Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu
 65 70 75 80
 Lys Val Lys Glu Val Glu Ala Glu Asp Ala Gly Val Tyr Val Cys Lys
 85 90 95
 Ala Thr Asn Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Ile Ile
 100 105 110
 Met

<210> 136
 <211> 148
 <212> DNA
 <213> Mouse

<400> 136
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgagatg atattagtcc aggaaggag agccctgggc caggtgggtc ttcggggggc 120
 caggaggacc cagccagcca gcagtggg 148

<210> 137
 <211> 49
 <212> PRT
 <213> Mouse

<400> 137

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Asp Asp Ile Ser Pro Gly Lys Glu Ser Pro
 20 25 30
 Gly Pro Gly Gly Ser Ser Gly Gly Gln Glu Asp Pro Ala Ser Gln Gln
 35 40 45
 Trp

<210> 138
 <211> 352
 <212> DNA
 <213> Mouse

<400> 138
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgagcac ggctcgtt cacacagccc tccaagatga ggcgccgagt gattgcacgg 120
 cctgtgggta gctctgtgcg gctcaagtgt gtggccagtg ggcacccacg gccagacatc 180
 atgtggatga aggatgacca gaccttgacg catctagagg ctagtgaaca cagaaagaag 240
 aagtggacac tgagcttgaa gaacctgaag cctgaagaca gtggcaagta cacgtgccgt 300
 gtatctaaca aggccggtgc catcaacgcc acctacaaag tggatgtaat cc 352

<210> 139
 <211> 117
 <212> PRT
 <213> Mouse

<400> 139

Met Thr Arg Ser Pro Ala Leu Leu Leu Leu Leu Leu Gly Ala Leu Pro
 1 5 10 15
 Ser Ala Glu Ala Ala Arg Ala Arg Pro Arg Phe Thr Gln Pro Ser Lys
 20 25 30
 Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser Val Arg Leu
 35 40 45
 Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Met Trp Met Lys
 50 55 60
 Asp Asp Gln Thr Leu Thr His Leu Glu Ala Ser Glu His Arg Lys Lys
 65 70 75 80
 Lys Trp Thr Leu Ser Leu Lys Asn Leu Lys Pro Glu Asp Ser Gly Lys
 85 90 95
 Tyr Thr Cys Arg Val Ser Asn Lys Ala Gly Ala Ile Asn Ala Thr Tyr
 100 105 110
 Lys Val Asp Val Ile
 115

<210> 140
 <211> 421
 <212> DNA
 <213> Mouse

<400> 140
 atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg 60
 gcgcgagagc ggactcgttc caagcctgtg ctcacagggg cacaccctgt gaacacaacg 120
 gtggacttcg gtgggacaac gtccttccag tgcaaggtgc gcagtgacgt gaagcctgtg 180
 atccagtggc tgaagcgggt ggagtacggc tccgaggagc gccacaactc caccattgat 240
 gtgggtggcc agaagtttgt ggtgttgccc acgggtgatg tgtgggtcacg gcctgatggc 300

tcctacctca acaagctgct catctctcgg gcccgccagg atgatgctgg catgtacatc	360
tgcctaggtg caaataccat gggctacagt ttccgtagcg ccttcctcac tgtattacca	420
g	421

<210> 141
 <211> 140
 <212> PRT
 <213> Mouse

<400> 141

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5					10					15	
Ser	Ala	Glu	Ala	Ala	Arg	Glu	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr
			20					25					30		
Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser
		35					40					45			
Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu
	50					55					60				
Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp
65					70				75					80	
Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser
			85					90					95		
Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg	Ala	Arg
			100					105					110		
Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly
		115					120					125			
Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro				
	130					135					140				

<210> 142
 <211> 67
 <212> DNA
 <213> Mouse

<400> 142	
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg	60
gcgcgag	67

<210> 143
 <211> 22
 <212> PRT
 <213> Mouse

<400> 143

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5					10				15	
Ser	Ala	Glu	Ala	Ala	Arg									
			20											

<210> 144
 <211> 1389
 <212> DNA
 <213> Mouse

<400> 144	
atgacgcgga gccccgcgct gctgctgctg ctattggggg ccctcccgtc ggctgaggcg	60
gcgcgaggac cccaagaat ggcagacaaa gtgggtcccac ggcagggtggc ccgcctgggc	120

cgcactgtgc	ggctacagtg	cccagtggag	ggggacccac	caccgttgac	catgtggacc	180
aaagatggcc	gcacaatcca	cagtggctgg	agccgcttcc	gtgtgctgcc	ccaggggtctg	240
aaggtgaagg	aggtggaggc	cgaggatgcc	ggtgtttatg	tgtgcaaggc	caccaatggc	300
tttggcagcc	tcagcgtcaa	ctacactctc	atcatgtgga	tgaaggatga	ccagaccttg	360
acgcatctag	aggctagtga	acacagaaag	aagaagtgga	cactgagctt	gaagaacctg	420
aagcctgaag	acagtggcaa	gtacacgtgc	cgtgtatcta	acaaggccgg	tgccatcaac	480
gccacctaca	aagtggatgt	aatccagcgg	actcgttcca	agcctgtgct	cacagggaca	540
caccctgtga	acacaacggc	ggacttcggt	gggacaacgt	ccttccagtg	caaggtgcgc	600
agtgacgtga	agcctgtgat	ccagtggctg	aagcgggtgg	agtacggctc	cgagggacgc	660
cacaactcca	ccattgatgt	gggtggccag	aagtttgtgg	tgttgcccac	gggtgatgtg	720
tggtcacggc	ctgatggctc	ctacctcaac	aagctgctca	tctctcgggc	ccgccaggat	780
gatgctggca	tgtacacctg	cctaggtgca	aataccatgg	gctacagttt	ccgtagcgcc	840
ttcctcactg	tattaccaga	ccccaaacct	ccagggcctc	ctatggcttc	ttcatcgtca	900
tccacaagcc	tgccatggcc	tgtggtgatc	ggcatcccag	ctggtgctgt	cttcataccta	960
ggcactgtgc	tgctctggct	ttgccagacc	aagaagaagc	catgtgcccc	agcatctaca	1020
cttcctgtgc	ctgggcatcg	tccccagggg	acatcccagag	aacgcagtgg	tgacaaggac	1080
ctgccctcat	tggctgtggg	catatgtgag	gagcatggat	ccgccatggc	cccccagcac	1140
atcctggcct	ctggctcaac	tgctggcccc	aagctgtacc	ccaagctata	cacagatgtg	1200
cacacacaca	cacatacaca	cacctgcact	cacacgctct	catgtggagg	gcaaggttca	1260
tcaacaccag	catgtccact	atcagtgcta	aatacagcga	atctccaagc	actgtgtcct	1320
gaggtaggca	tatggggggc	aaggcaacag	gttggggagaa	ttgagaacaa	tggaggaaga	1380
gtatcttag						1389

<210> 145

<211> 462

<212> PRT

<213> Mouse

<400> 145

Met	Thr	Arg	Ser	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Gly	Ala	Leu	Pro
1				5				10					15	
Ser	Ala	Glu	Ala	Ala	Arg	Gly	Pro	Pro	Arg	Met	Ala	Asp	Lys	Val
			20					25					30	Val
Pro	Arg	Gln	Val	Ala	Arg	Leu	Gly	Arg	Thr	Val	Arg	Leu	Gln	Cys
		35					40					45		Pro
Val	Glu	Gly	Asp	Pro	Pro	Pro	Leu	Thr	Met	Trp	Thr	Lys	Asp	Gly
	50					55					60			Arg
Thr	Ile	His	Ser	Gly	Trp	Ser	Arg	Phe	Arg	Val	Leu	Pro	Gln	Gly
65					70				75					80
Lys	Val	Lys	Glu	Val	Glu	Ala	Glu	Asp	Ala	Gly	Val	Tyr	Val	Cys
			85					90					95	Lys
Ala	Thr	Asn	Gly	Phe	Gly	Ser	Leu	Ser	Val	Asn	Tyr	Thr	Leu	Ile
			100					105					110	Met
Trp	Met	Lys	Asp	Asp	Gln	Thr	Leu	Thr	His	Leu	Glu	Ala	Ser	Glu
	115						120					125		His
Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser	Leu	Lys	Asn	Leu	Lys	Pro	Glu
	130					135					140			Asp
Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val	Ser	Asn	Lys	Ala	Gly	Ala	Ile
145					150				155					160
Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile	Gln	Arg	Thr	Arg	Ser	Lys	Pro
			165					170					175	Val
Leu	Thr	Gly	Thr	His	Pro	Val	Asn	Thr	Thr	Val	Asp	Phe	Gly	Gly
		180					185						190	Thr
Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg	Ser	Asp	Val	Lys	Pro	Val	Ile
	195						200					205		Gln
Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly	Ser	Glu	Gly	Arg	His	Asn	Ser
	210					215					220			Thr

Ile	Asp	Val	Gly	Gly	Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val
225					230					235					240
Trp	Ser	Arg	Pro	Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Ser	Arg
				245					250					255	
Ala	Arg	Gln	Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr
			260				265						270		
Met	Gly	Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro
	275					280						285			
Lys	Pro	Pro	Gly	Pro	Pro	Met	Ala	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Leu
	290					295					300				
Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	Leu
305					310					315					320
Gly	Thr	Val	Leu	Leu	Trp	Leu	Cys	Gln	Thr	Lys	Lys	Lys	Pro	Cys	Ala
			325					330						335	
Pro	Ala	Ser	Thr	Leu	Pro	Val	Pro	Gly	His	Arg	Pro	Pro	Gly	Thr	Ser
			340					345					350		
Arg	Glu	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	Ala	Val	Gly	Ile
	355					360						365			
Cys	Glu	Glu	His	Gly	Ser	Ala	Met	Ala	Pro	Gln	His	Ile	Leu	Ala	Ser
	370					375					380				
Gly	Ser	Thr	Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Val
385					390					395					400
His	Thr	His	Thr	His	Thr	His	Thr	Cys	Thr	His	Thr	Leu	Ser	Cys	Gly
			405					410						415	
Gly	Gln	Gly	Ser	Ser	Thr	Pro	Ala	Cys	Pro	Leu	Ser	Val	Leu	Asn	Thr
			420					425					430		
Ala	Asn	Leu	Gln	Ala	Leu	Cys	Pro	Glu	Val	Gly	Ile	Trp	Gly	Pro	Arg
	435						440					445			
Gln	Gln	Val	Gly	Arg	Ile	Glu	Asn	Asn	Gly	Gly	Arg	Val	Ser		
	450					455					460				